



09 04 03 23 06 10 02

# 8

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.
- (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS
- (iii) NUMBER OF SEQUENCES: 165
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: MEDLEN & CARROLL
  - (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
  - (C) CITY: SAN FRANCISCO
  - (D) STATE: CALIFORNIA
  - (E) COUNTRY: UNITED STATES OF AMERICA
  - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: CARROLL, PETER G.
  - (B) REGISTRATION NUMBER: 32,837
  - (C) REFERENCE/DOCKET NUMBER: FORS-01756
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 705-8410
  - (B) TELEFAX: (415) 397-8338

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2506 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

TACAAGGCGG	GCCGGGCCCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCCTGGCCA	GCCTGGCCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCACC	420
GCCGACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCCTCCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCGA	CCAGTGGGCC	540
GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCCAA	GGTGCGCACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAGC	CCCAAGGCCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCCAT	GTGGGCCGAT	960
CTTCTGGCCC	TGGCCGCCGC	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCTGGCC	1080
CTGAGGGAAG	GCCTTGGCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCGGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCGC	CCTTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCCT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTCC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCCTGGAG	1560
GCCCTCCGCG	AGGCCACCCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCAGGAC	GGGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
CTCCAGAACA	TCCCCGTCCG	CACCCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCCAGG	AGGGGCGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGGCGTCCCC	CGGGAGGCCG	TGGACCCCTT	GATGCGCCGG	1980
GCGGCCAAGA	CCATCAACTT	CGGGGTCCTC	TACGGCATGT	CGGCCACCG	CCTCTCCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100

CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 2160  
GAGACCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG 2220  
CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCCTCC AGGGCACCGC CGCCGACCTC 2280  
ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC 2340  
CTTCAGGTCC ACGACGAGCT GGTCTCTGAG GCCC AAAAG AGAGGGCGGA GGCCGTGGCC 2400  
CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG 2460  
GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC TTCCCCTCTT TGAGCCCAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 60  
CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTCACCA CCAGCCGCGG CGAACCCGTT 120  
CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCC TGAAGGAGGA CGGGGACGTG 180  
GTGGTGGTGG TCTTTGACGC CAAGGCCCC TCCTTCCGCC ACGAGGCCTA CGAGGCCTAC 240  
AAGGCGGGCC GGGCCCCAC CCCGGAGGAC TTTCCCCGGC AGCTGGCCCT CATCAAGGAG 300  
TTGGTGGACC TCCTAGGCCT TGTGCGGCTG GAGGTTCCCG GCTTTGAGGC GGACGACGTG 360  
CTGGCCACCC TGGCCAAGCG GCGGAAAAG GAGGGGTACG AGGTGCGCAT CCTCACTGCC 420  
GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACCC TGAGGGGTAC 480  
CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC 540  
TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG 600  
AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG 660  
GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT 720  
TCCCGGAAGC TTTCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGACTT CGGGAGGCGC 780  
CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTGGAGC GGTGAGTT TGGAAGCCTC 840  
CTCCACGAGT TCGGCCTCCT GGAGGGGCGG AAGGCGGCAG AGGAGGCCCC CTGGCCCCCT 900  
CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCCG AGCCCATGTG GGCCGAGCTT 960  
CTGGCCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC 1020  
CTGAGGGACC TTAAGGGGGT GCGGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG 1080

CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140
CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCACCTG	1740
CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
CTTTCCATCC CCTACGAGGA GCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC	2220
GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTAGGAAC TGGGGGCGAG GATGCTTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC	180
AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360
GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC	420
ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG	480
GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG	540
GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG	660
AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC	720
CTCAGGCTCT CCTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC	780
GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC	840
GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCCTGGA GGAGGCCCCC	900
TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCTCTT CCCGCCCCGA GCCCATGTGG	960
GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC	1020
TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC	1080
TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC	1140
CTCCTGGACC CCTCCAACAC CACCCCCGAG GGGGTGGCGC GGCCTACGG GGGGGAGTGG	1200
ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG	1260
CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC	1320
CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC	1380
CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG	1440
GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT	1500
AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG	1560
CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC	1620
ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC	1680
CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC	1740
CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC	1800

GTGGCCGAGG	CGGGTTGGGC	GTTGGTGGCC	CTGGACTATA	GCCAGATAGA	GCTCCGCGTC	1860
CTCGCCCACC	TCTCCGGGGA	CGAAAACCTG	ATCAGGGTCT	TCCAGGAGGG	GAAGGACATC	1920
CACACCCAGA	CCGCAAGCTG	GATGTTCTGGC	GTCCCCCCGG	AGGCCGTGGA	CCCCCTGATG	1980
CGCCGGGCGG	CCAAGACGGT	GAACTTCGGC	GTCCTCTACG	GCATGTCCGC	CCATAGGCTC	2040
TCCCAGGAGC	TTGCCATCCC	CTACGAGGAG	GCGGTGGCCT	TTATAGAGGC	TACTTCCAAA	2100
GCTTCCCCAA	GGTGCGGGCC	TGGATAGAAA	AGACCCTGGA	GGAGGGGAGG	AAGCGGGGCT	2160
ACGTGGA AAC	CCTCTTCGGA	AGAAGGCGCT	ACGTGCCCCG	CCTCAACGCC	CGGGTGAAGA	2220
GCGTCAGGGA	GGCCGCGGAG	CGCATGGCCT	TCAACATGCC	CGTCCAGGGC	ACCGCCGCCG	2280
ACCTCATGAA	GCTCGCCATG	GTGAAGCTCT	TCCCCCGCCT	CCGGGAGATG	GGGGCCCGCA	2340
TGCTCCTCCA	GGTCCACGAC	GAGCTCCTCC	TGGAGGCCCC	CCAAGCGCGG	GCCGAGGAGG	2400
TGGCGGCTTT	GGCCAAGGAG	GCCATGGAGA	AGGCCTATCC	CCTCGCCGTG	CCCCTGGAGG	2460
TGGAGGTGGG	GATGGGGGAG	GACTGGCTTT	CCGCCAAGGG	TTAG		2504

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1	Arg	Gly	Met	Leu 5	Pro	Leu	Phe	Glu	Pro 10	Lys	Gly	Arg	Val	Leu 15	Leu
Val	Asp	Gly	His 20	His	Leu	Ala	Tyr	Arg 25	Thr	Phe	His	Ala	Leu 30	Lys	Gly
Leu	Thr	Thr 35	Ser	Arg	Gly	Glu	Pro 40	Val	Gln	Ala	Val	Tyr 45	Gly	Phe	Ala
Lys	Ser 50	Leu	Leu	Lys	Ala	Leu 55	Lys	Glu	Asp	Gly	Asp 60	Ala	Val	Ile	Val
Val 65	Phe	Asp	Ala	Lys	Ala 70	Pro	Ser	Phe	Arg	His 75	Glu	Ala	Tyr	Gly	Gly 80
Tyr	Lys	Ala	Gly	Arg 85	Ala	Pro	Thr	Pro	Glu 90	Asp	Phe	Pro	Arg	Gln 95	Leu
Ala	Leu	Ile	Lys 100	Glu	Leu	Val	Asp	Leu 105	Leu	Gly	Leu	Ala	Arg 110	Leu	Glu
Val	Pro	Gly 115	Tyr	Glu	Ala	Asp	Asp 120	Val	Leu	Ala	Ser	Leu 125	Ala	Lys	Lys
Ala	Glu 130	Lys	Glu	Gly	Tyr	Glu 135	Val	Arg	Ile	Leu	Thr 140	Ala	Asp	Lys	Asp

Leu 145	Tyr	Gln	Leu	Leu	Ser 150	Asp	Arg	Ile	His	Val 155	Leu	His	Pro	Glu	Gly 160
Tyr	Leu	Ile	Thr	Pro 165	Ala	Trp	Leu	Trp	Glu 170	Lys	Tyr	Gly	Leu	Arg 175	Pro
Asp	Gln	Trp	Ala 180	Asp	Tyr	Arg	Ala	Leu 185	Thr	Gly	Asp	Glu	Ser 190	Asp	Asn
Leu	Pro	Gly 195	Val	Lys	Gly	Ile	Gly 200	Glu	Lys	Thr	Ala	Arg 205	Lys	Leu	Leu
Glu	Glu 210	Trp	Gly	Ser	Leu	Glu 215	Ala	Leu	Leu	Lys	Asn 220	Leu	Asp	Arg	Leu
Lys 225	Pro	Ala	Ile	Arg	Glu 230	Lys	Ile	Leu	Ala	His 235	Met	Asp	Asp	Leu	Lys 240
Leu	Ser	Trp	Asp	Leu 245	Ala	Lys	Val	Arg	Thr 250	Asp	Leu	Pro	Leu	Glu 255	Val
Asp	Phe	Ala	Lys 260	Arg	Arg	Glu	Pro	Asp 265	Arg	Glu	Arg	Leu	Arg 270	Ala	Phe
Leu	Glu	Arg 275	Leu	Glu	Phe	Gly	Ser 280	Leu	Leu	His	Glu	Phe 285	Gly	Leu	Leu
Glu	Ser 290	Pro	Lys	Ala	Leu	Glu 295	Glu	Ala	Pro	Trp	Pro 300	Pro	Pro	Glu	Gly
Ala 305	Phe	Val	Gly	Phe	Val 310	Leu	Ser	Arg	Lys	Glu 315	Pro	Met	Trp	Ala	Asp 320
Leu	Leu	Ala	Leu	Ala 325	Ala	Ala	Arg	Gly	Gly 330	Arg	Val	His	Arg	Ala 335	Pro
Glu	Pro	Tyr	Lys 340	Ala	Leu	Arg	Asp	Leu 345	Lys	Glu	Ala	Arg	Gly 350	Leu	Leu
Ala	Lys	Asp 355	Leu	Ser	Val	Leu	Ala 360	Leu	Arg	Glu	Gly	Leu 365	Gly	Leu	Pro
Pro	Gly 370	Asp	Asp	Pro	Met	Leu 375	Leu	Ala	Tyr	Leu	Leu 380	Asp	Pro	Ser	Asn
Thr 385	Thr	Pro	Glu	Gly	Val 390	Ala	Arg	Arg	Tyr	Gly 395	Gly	Glu	Trp	Thr	Glu 400
Glu	Ala	Gly	Glu	Arg 405	Ala	Ala	Leu	Ser	Glu 410	Arg	Leu	Phe	Ala	Asn 415	Leu
Trp	Gly	Arg	Leu 420	Glu	Gly	Glu	Glu	Arg 425	Leu	Leu	Trp	Leu	Tyr 430	Arg	Glu
Val	Glu	Arg 435	Pro	Leu	Ser	Ala	Val 440	Leu	Ala	His	Met	Glu 445	Ala	Thr	Gly
Val	Arg 450	Leu	Asp	Val	Ala	Tyr 455	Leu	Arg	Ala	Leu	Ser 460	Leu	Glu	Val	Ala
Glu 465	Glu	Ile	Ala	Arg	Leu	Glu 470	Ala	Glu	Val	Phe 475	Arg	Leu	Ala	Gly	His 480



Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp
				485					490					495	
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg
			500					505					510		
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile
		515					520					525			
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr
	530					535					540				
Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu
545					550					555					560
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser
				565					570					575	
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln
			580					585					590		
Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala
		595					600					605			
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly
	610					615					620				
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr
625					630					635					640
Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro
				645					650					655	
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly
			660					665					670		
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu
		675					680					685			
Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
	690					695					700				
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val
705					710					715					720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
	770					775					780				



[illegible]

Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790					795					800
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu
			820					825					830		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met 1	Ala	Met	Leu	Pro 5	Leu	Phe	Glu	Pro	Lys 10	Gly	Arg	Val	Leu	Leu 15	Val
Asp	Gly	His	His 20	Leu	Ala	Tyr	Arg	Thr 25	Phe	Phe	Ala	Leu	Lys 30	Gly	Leu
Thr	Thr	Ser 35	Arg	Gly	Glu	Pro	Val 40	Gln	Ala	Val	Tyr	Gly 45	Phe	Ala	Lys
Ser	Leu 50	Leu	Lys	Ala	Leu	Lys 55	Glu	Asp	Gly	Asp	Val 60	Val	Val	Val	Val
Phe 65	Asp	Ala	Lys	Ala	Pro 70	Ser	Phe	Arg	His	Glu 75	Ala	Tyr	Glu	Ala	Tyr 80
Lys	Ala	Gly	Arg	Ala 85	Pro	Thr	Pro	Glu	Asp 90	Phe	Pro	Arg	Gln	Leu 95	Ala
Leu	Ile	Lys	Glu 100	Leu	Val	Asp	Leu	Leu 105	Gly	Leu	Val	Arg	Leu 110	Glu	Val
Pro	Gly	Phe 115	Glu	Ala	Asp	Asp	Val 120	Leu	Ala	Thr	Leu	Ala 125	Lys	Arg	Ala
Glu	Lys 130	Glu	Gly	Tyr	Glu	Val 135	Arg	Ile	Leu	Thr	Ala 140	Asp	Arg	Asp	Leu
Tyr 145	Gln	Leu	Leu	Ser	Glu 150	Arg	Ile	Ala	Ile	Leu 155	His	Pro	Glu	Gly	Tyr 160
Leu	Ile	Thr	Pro	Ala 165	Trp	Leu	Tyr	Glu	Lys 170	Tyr	Gly	Leu	Arg	Pro 175	Glu
Gln	Trp	Val	Asp 180	Tyr	Arg	Ala	Leu	Ala 185	Gly	Asp	Pro	Ser	Asp 190	Asn	Ile
Pro	Gly	Val 195	Lys	Gly	Ile	Gly	Glu 200	Lys	Thr	Ala	Gln	Arg 205	Leu	Ile	Arg

Glu 210	Trp	Gly	Ser	Leu	Glu 215	Asn	Leu	Phe	Gln	His	Leu 220	Asp	Gln	Val	Lys
Pro 225	Ser	Leu	Arg	Glu	Lys 230	Leu	Gln	Ala	Gly	Met 235	Glu	Ala	Leu	Ala	Leu 240
Ser	Arg	Lys	Leu	Ser 245	Gln	Val	His	Thr	Asp 250	Leu	Pro	Leu	Glu	Val 255	Asp
Phe	Gly	Arg	Arg 260	Arg	Thr	Pro	Asn	Leu 265	Glu	Gly	Leu	Arg	Ala 270	Phe	Leu
Glu	Arg	Leu 275	Glu	Phe	Gly	Ser	Leu 280	Leu	His	Glu	Phe	Gly 285	Leu	Leu	Glu
Gly	Pro 290	Lys	Ala	Ala	Glu	Glu 295	Ala	Pro	Trp	Pro	Pro 300	Pro	Glu	Gly	Ala
Phe 305	Leu	Gly	Phe	Ser	Phe 310	Ser	Arg	Pro	Glu	Pro 315	Met	Trp	Ala	Glu	Leu 320
Leu	Ala	Leu	Ala	Gly 325	Ala	Trp	Glu	Gly	Arg 330	Leu	His	Arg	Ala	Gln 335	Asp
Pro	Leu	Arg	Gly 340	Leu	Arg	Asp	Leu	Lys 345	Gly	Val	Arg	Gly	Ile 350	Leu	Ala
Lys	Asp	Leu 355	Ala	Val	Leu	Ala	Leu 360	Arg	Glu	Gly	Leu	Asp 365	Leu	Phe	Pro
Glu	Asp 370	Asp	Pro	Met	Leu	Leu 375	Ala	Tyr	Leu	Leu	Asp 380	Pro	Ser	Asn	Thr
Thr 385	Pro	Glu	Gly	Val	Ala 390	Arg	Arg	Tyr	Gly	Gly 395	Glu	Trp	Thr	Glu	Asp 400
Ala	Gly	Glu	Arg	Ala 405	Leu	Leu	Ala	Glu	Arg 410	Leu	Phe	Gln	Thr	Leu 415	Lys
Glu	Arg	Leu	Lys 420	Gly	Glu	Glu	Arg	Leu 425	Leu	Trp	Leu	Tyr	Glu 430	Glu	Val
Glu	Lys	Pro 435	Leu	Ser	Arg	Val	Leu 440	Ala	Arg	Met	Glu	Ala 445	Thr	Gly	Val
Arg	Leu 450	Asp	Val	Ala	Tyr	Leu 455	Gln	Ala	Leu	Ser	Leu 460	Glu	Val	Glu	Ala
Glu 465	Val	Arg	Gln	Leu	Glu 470	Glu	Glu	Val	Phe	Arg 475	Leu	Ala	Gly	His	Pro 480
Phe	Asn	Leu	Asn	Ser 485	Arg	Asp	Gln	Leu	Glu 490	Arg	Val	Leu	Phe	Asp 495	Glu
Leu	Gly	Leu	Pro 500	Ala	Ile	Gly	Lys	Thr 505	Glu	Lys	Thr	Gly	Lys 510	Arg	Ser
Thr	Ser	Ala 515	Ala	Val	Leu	Glu	Ala 520	Leu	Arg	Glu	Ala	His 525	Pro	Ile	Val
Asp	Arg 530	Ile	Leu	Gln	Tyr	Arg 535	Glu	Leu	Thr	Lys	Leu 540	Lys	Asn	Thr	Tyr

Ile 545	Asp	Pro	Leu	Pro	Ala 550	Leu	Val	His	Pro	Lys 555	Thr	Gly	Arg	Leu	His 560
Thr	Arg	Phe	Asn	Gln 565	Thr	Ala	Thr	Ala	Thr 570	Gly	Arg	Leu	Ser	Ser 575	Ser
Asp	Pro	Asn	Leu 580	Gln	Asn	Ile	Pro	Val 585	Arg	Thr	Pro	Leu	Gly 590	Gln	Arg
Ile	Arg	Arg 595	Ala	Phe	Val	Ala	Glu 600	Glu	Gly	Trp	Val	Leu 605	Val	Val	Leu
Asp	Tyr 610	Ser	Gln	Ile	Glu	Leu 615	Arg	Val	Leu	Ala	His 620	Leu	Ser	Gly	Asp
Glu 625	Asn	Leu	Ile	Arg	Val 630	Phe	Gln	Glu	Gly	Arg 635	Asp	Ile	His	Thr	Gln 640
Thr	Ala	Ser	Trp	Met 645	Phe	Gly	Val	Ser	Pro 650	Glu	Gly	Val	Asp	Pro 655	Leu
Met	Arg	Arg	Ala 660	Ala	Lys	Thr	Ile	Asn 665	Phe	Gly	Val	Leu	Tyr 670	Gly	Met
Ser	Ala	His 675	Arg	Leu	Ser	Gly	Glu 680	Leu	Ser	Ile	Pro	Tyr 685	Glu	Glu	Ala
Val	Ala 690	Phe	Ile	Glu	Arg	Tyr 695	Phe	Gln	Ser	Tyr	Pro 700	Lys	Val	Arg	Ala
Trp 705	Ile	Glu	Gly	Thr	Leu 710	Glu	Glu	Gly	Arg	Arg 715	Arg	Gly	Tyr	Val	Glu 720
Thr	Leu	Phe	Gly	Arg 725	Arg	Arg	Tyr	Val	Pro 730	Asp	Leu	Asn	Ala	Arg 735	Val
Lys	Ser	Val	Arg 740	Glu	Ala	Ala	Glu	Arg 745	Met	Ala	Phe	Asn	Met 750	Pro	Val
Gln	Gly	Thr 755	Ala	Ala	Asp	Leu	Met 760	Lys	Leu	Ala	Met	Val 765	Arg	Leu	Phe
Pro	Arg 770	Leu	Gln	Glu	Leu	Gly 775	Ala	Arg	Met	Leu	Leu 780	Gln	Val	His	Asp
Glu 785	Leu	Val	Leu	Glu	Ala 790	Pro	Lys	Asp	Arg	Ala 795	Glu	Arg	Val	Ala	Ala 800
Leu	Ala	Lys	Glu	Val 805	Met	Glu	Gly	Val	Trp 810	Pro	Leu	Gln	Val	Pro 815	Leu
Glu	Val	Glu	Val 820	Gly	Leu	Gly	Glu	Asp 825	Trp	Leu	Ser	Ala	Lys 830	Glu	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met 1	Glu	Ala	Met	Leu 5	Pro	Leu	Phe	Glu	Pro 10	Lys	Gly	Arg	Val	Leu 15	Leu
Val	Asp	Gly	His 20	His	Leu	Ala	Tyr	Arg 25	Thr	Phe	Phe	Ala	Leu 30	Lys	Gly
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro 40	Val	Gln	Ala	Val	Tyr 45	Gly	Phe	Ala
Lys	Ser 50	Leu	Leu	Lys	Ala	Leu 55	Lys	Glu	Asp	Gly	Tyr 60	Lys	Ala	Val	Phe
Val 65	Val	Phe	Asp	Ala	Lys 70	Ala	Pro	Ser	Phe	Arg 75	His	Glu	Ala	Tyr	Glu 80
Ala	Tyr	Lys	Ala	Gly 85	Arg	Ala	Pro	Thr	Pro 90	Glu	Asp	Phe	Pro	Arg 95	Gln
Leu	Ala	Leu	Ile 100	Lys	Glu	Leu	Val	Asp 105	Leu	Leu	Gly	Phe	Thr 110	Arg	Leu
Glu	Val	Pro 115	Gly	Tyr	Glu	Ala	Asp 120	Asp	Val	Leu	Ala	Thr 125	Leu	Ala	Lys
Lys	Ala 130	Glu	Lys	Glu	Gly	Tyr 135	Glu	Val	Arg	Ile	Leu 140	Thr	Ala	Asp	Arg
Asp 145	Leu	Tyr	Gln	Leu	Val 150	Ser	Asp	Arg	Val	Ala 155	Val	Leu	His	Pro	Glu 160
Gly	His	Leu	Ile	Thr 165	Pro	Glu	Trp	Leu	Trp 170	Glu	Lys	Tyr	Gly	Leu 175	Arg
Pro	Glu	Gln	Trp 180	Val	Asp	Phe	Arg	Ala 185	Leu	Val	Gly	Asp	Pro 190	Ser	Asp
Asn	Leu	Pro 195	Gly	Val	Lys	Gly	Ile 200	Gly	Glu	Lys	Thr	Ala 205	Leu	Lys	Leu
Leu	Lys 210	Glu	Trp	Gly	Ser	Leu 215	Glu	Asn	Leu	Leu	Lys 220	Asn	Leu	Asp	Arg
Val 225	Lys	Pro	Glu	Asn	Val 230	Arg	Glu	Lys	Ile	Lys 235	Ala	His	Leu	Glu	Asp 240
Leu	Arg	Leu	Ser	Leu 245	Glu	Leu	Ser	Arg	Val 250	Arg	Thr	Asp	Leu	Pro 255	Leu
Glu	Val	Asp	Leu 260	Ala	Gln	Gly	Arg	Glu 265	Pro	Asp	Arg	Glu	Gly 270	Leu	Arg
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe 280	Gly	Ser	Leu	Leu	His 285	Glu	Phe	Gly
Leu	Leu 290	Glu	Ala	Pro	Ala	Pro 295	Leu	Glu	Glu	Ala	Pro 300	Trp	Pro	Pro	Pro

[illegible]

Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro	Leu 340	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly	Glu 425	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr	Gly 450	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro 530	Ile	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560
Arg	Leu	His	Thr 565	Arg	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
770 775 780

Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
820 825 830

Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC	180
NNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360

GACGTNCTGG	CCACCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAGCTCCTT	TCCGACCGCA	TCGCCGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	GTGGCTTTGG	GAGAAGTACG	GCCTGAGGCC	GGAGCAGTGG	540
GTGGACTACC	GGGCCCTGGC	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCNGAA	GCTCCTCNAG	GAGTGGGGGA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTGAAGCC	CGCCNTCCGG	GAGAAGATCC	AGGCCCACAT	GGANGACCTG	720
ANGCTCTCCT	GGGAGCTNTC	CCAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAGNGGCGGG	AGCCCGACCG	GGAGGGGCTT	AGGGCCTTTC	TGGAGAGGCT	GGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTCCTGGAG	GGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTCCTTTCCC	GCCCCGAGCC	CATGTGGGCC	960
GAGCTTCTGG	CCCTGGCCGC	CGCCAGGGAG	GGCCGGGTCC	ACCGGGCACC	AGACCCCTTT	1020
ANGGGCCTNA	GGGACCTNAA	GGAGGTGCGG	GGNCTCCTCG	CCAAGGACCT	GGCCGTTTTG	1080
GCCCTGAGGG	AGGGCCTNGA	CCTCNTGCCC	GGGGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGGGG	GGAGTGGACG	1200
GAGGANGCGG	GGGAGCGGGC	CCTCCTNTCC	GAGAGGCTCT	TCCNGAACCT	NNNGCAGCGC	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCAGGAGG	TGGAGAAGCC	CCTTTCCCGG	1320
GTCCTGGCCC	ACATGGAGGC	CACGGGGGTN	CGGCTGGACG	TGGCCTACCT	CCAGGCCCTN	1380
TCCCTGGAGG	TGGCGGAGGA	GATCCGCCGC	CTCGAGGAGG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TGCTCTTTGA	CGAGCTNGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACN	GGCAAGCGCT	CCACCAGCGC	CGCCGTGCTG	1560
GAGGCCCTNC	GNGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTCAAGA	ACACCTACAT	NGACCCCTTG	CCNGNCCTCG	TCCACCCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTTAGTAG	CTCCGACCCC	1740
AACCTGCAGA	ACATCCCCGT	CCGCACCCCN	CTGGGCCAGA	GGATCCGCCG	GGCCTTCGTG	1800
GCCGAGGAGG	GNTGGGTGTT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CCGGGTCTCTG	1860
GCCCACCTCT	CCGGGGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGAG	GGACATCCAC	1920
ACCCAGACCG	CCAGCTGGAT	GTTTCGGCGTC	CCCCCGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCCGCCCA	CCGCCTCTCC	2040
CAGGAGCTTG	CCATCCCCTA	CGAGGAGGCG	GTGGCCTTCA	TTGAGCGCTA	CTTCCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGGCGCTAC	GTGCCCCGACC	TCAACGCCCG	GGTGAAGAGC	2220



[illegible]

GTGCGGGAGG	CGGCGGAGCG	CATGGCCTTC	AACATGCCCCG	TCCAGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCCATGGT	GAAGCTCTTC	CCCCGGCTNC	AGGAAATGGG	GGCCAGGATG	2340
CTCCTNCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCCCA	AAGAGCGGGC	GGAGGNGGTG	2400
GCCGCTTTGG	CCAAGGAGGT	CATGGAGGGG	GTCTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TGGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	AG		2502

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "Xaa at this position can be
no acid."
```

(ix) FEATURE:

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 63
(D) OTHER INFORMATION: /note= "Xaa at this position can be
no acid."
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(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 109  
(D) OTHER INFORMATION: /note= "Xaa at this position can be no acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 186  
(D) OTHER INFORMATION: /note= "Xaa at this position can be no acid."

(ix) FEATURE:

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 205
(D) OTHER INFORMATION: /note= "Xaa at this position can be
no acid."
```

(ix) FEATURE :

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 209
(D) OTHER INFORMATION: /note= "Xaa at this position can be
no acid."
```

(ix) FEATURE :

- ```
(A) NAME/KEY: Modified-site
(B) LOCATION: 227..228
(D) OTHER INFORMATION: /note= "Xaa at these positions can
be any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 233
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 240
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 243..244
      (D) OTHER INFORMATION: /note= "Xaa at these positions can
be any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 247
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 260
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 290
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 329
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 336
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 340
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 368
      (D) OTHER INFORMATION: /note= "Xaa at this position can be
any amino acid."
```

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 414  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 417..418  
 (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 431  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 551  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 605  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 773  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 794  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 798  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 823  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 833  
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Ala | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | Leu | 1   | 5   | 10  | 15  |
| Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | Phe | Ala | Leu | Lys | Gly | 20  | 25  | 30  |     |
| Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | Ala | 35  | 40  | 45  |     |
| Lys | Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Ala | Val | Xaa | Val | 50  | 55  | 60  |     |
| Val | Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Glu | Ala | 65  | 70  | 75  | 80  |
| Tyr | Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | Leu | 85  | 90  | 95  |     |
| Ala | Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Xaa | Arg | Leu | Glu | 100 | 105 | 110 |     |
| Val | Pro | Gly | Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Thr | Leu | Ala | Lys | Lys | 115 | 120 | 125 |     |
| Ala | Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Arg | Asp | 130 | 135 | 140 |     |
| Leu | Tyr | Gln | Leu | Leu | Ser | Asp | Arg | Ile | Ala | Val | Leu | His | Pro | Glu | Gly | 145 | 150 | 155 | 160 |
| Tyr | Leu | Ile | Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | Pro | 165 | 170 | 175 |     |
| Glu | Gln | Trp | Val | Asp | Tyr | Arg | Ala | Leu | Xaa | Gly | Asp | Pro | Ser | Asp | Asn | 180 | 185 | 190 |     |
| Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Xaa | Lys | Leu | Leu | 195 | 200 | 205 |     |
| Xaa | Glu | Trp | Gly | Ser | Leu | Glu | Asn | Leu | Leu | Lys | Asn | Leu | Asp | Arg | Val | 210 | 215 | 220 |     |
| Lys | Pro | Xaa | Xaa | Arg | Glu | Lys | Ile | Xaa | Ala | His | Met | Glu | Asp | Leu | Xaa | 225 | 230 | 235 | 240 |
| Leu | Ser | Xaa | Xaa | Leu | Ser | Xaa | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | Val | 245 | 250 | 255 |     |
| Asp | Phe | Ala | Xaa | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Gly | Leu | Arg | Ala | Phe | 260 | 265 | 270 |     |
| Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | Leu | 275 | 280 | 285 |     |
| Glu | Xaa | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu | Gly | 290 | 295 | 300 |     |
| Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Pro | Glu | Pro | Met | Trp | Ala | Glu | 305 | 310 | 315 | 320 |

[illegible]

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu        | Leu        | Ala        | Leu        | Ala<br>325 | Ala        | Ala        | Arg        | Xaa        | Gly<br>330 | Arg        | Val        | His        | Arg        | Ala<br>335 | Xaa        |
| Asp        | Pro        | Leu        | Xaa<br>340 | Gly        | Leu        | Arg        | Asp        | Leu<br>345 | Lys        | Glu        | Val        | Arg        | Gly<br>350 | Leu        | Leu        |
| Ala        | Lys        | Asp<br>355 | Leu        | Ala        | Val        | Leu        | Ala<br>360 | Leu        | Arg        | Glu        | Gly        | Leu<br>365 | Asp        | Leu        | Xaa        |
| Pro        | Gly<br>370 | Asp        | Asp        | Pro        | Met        | Leu<br>375 | Leu        | Ala        | Tyr        | Leu        | Leu<br>380 | Asp        | Pro        | Ser        | Asn        |
| Thr<br>385 | Thr        | Pro        | Glu        | Gly        | Val<br>390 | Ala        | Arg        | Arg        | Tyr        | Gly<br>395 | Gly        | Glu        | Trp        | Thr        | Glu<br>400 |
| Asp        | Ala        | Gly        | Glu        | Arg<br>405 | Ala        | Leu        | Leu        | Ser        | Glu<br>410 | Arg        | Leu        | Phe        | Xaa        | Asn<br>415 | Leu        |
| Xaa        | Xaa        | Arg        | Leu<br>420 | Glu        | Gly        | Glu        | Glu        | Arg<br>425 | Leu        | Leu        | Trp        | Leu        | Tyr<br>430 | Xaa        | Glu        |
| Val        | Glu        | Lys<br>435 | Pro        | Leu        | Ser        | Arg        | Val<br>440 | Leu        | Ala        | His        | Met        | Glu<br>445 | Ala        | Thr        | Gly        |
| Val        | Arg<br>450 | Leu        | Asp        | Val        | Ala        | Tyr<br>455 | Leu        | Gln        | Ala        | Leu        | Ser<br>460 | Leu        | Glu        | Val        | Ala        |
| Glu<br>465 | Glu        | Ile        | Arg        | Arg        | Leu<br>470 | Glu        | Glu        | Glu        | Val        | Phe<br>475 | Arg        | Leu        | Ala        | Gly        | His<br>480 |
| Pro        | Phe        | Asn        | Leu        | Asn<br>485 | Ser        | Arg        | Asp        | Gln        | Leu<br>490 | Glu        | Arg        | Val        | Leu        | Phe<br>495 | Asp        |
| Glu        | Leu        | Gly        | Leu<br>500 | Pro        | Ala        | Ile        | Gly        | Lys<br>505 | Thr        | Glu        | Lys        | Thr        | Gly<br>510 | Lys        | Arg        |
| Ser        | Thr        | Ser<br>515 | Ala        | Ala        | Val        | Leu        | Glu<br>520 | Ala        | Leu        | Arg        | Glu        | Ala<br>525 | His        | Pro        | Ile        |
| Val        | Glu<br>530 | Lys        | Ile        | Leu        | Gln        | Tyr<br>535 | Arg        | Glu        | Leu        | Thr        | Lys<br>540 | Leu        | Lys        | Asn        | Thr        |
| Tyr<br>545 | Ile        | Asp        | Pro        | Leu        | Pro<br>550 | Xaa        | Leu        | Val        | His        | Pro<br>555 | Arg        | Thr        | Gly        | Arg        | Leu<br>560 |
| His        | Thr        | Arg        | Phe        | Asn<br>565 | Gln        | Thr        | Ala        | Thr        | Ala<br>570 | Thr        | Gly        | Arg        | Leu        | Ser<br>575 | Ser        |
| Ser        | Asp        | Pro        | Asn<br>580 | Leu        | Gln        | Asn        | Ile        | Pro<br>585 | Val        | Arg        | Thr        | Pro        | Leu<br>590 | Gly        | Gln        |
| Arg        | Ile        | Arg<br>595 | Arg        | Ala        | Phe        | Val        | Ala<br>600 | Glu        | Glu        | Gly        | Trp        | Xaa<br>605 | Leu        | Val        | Ala        |
| Leu        | Asp<br>610 | Tyr        | Ser        | Gln        | Ile        | Glu<br>615 | Leu        | Arg        | Val        | Leu        | Ala<br>620 | His        | Leu        | Ser        | Gly        |
| Asp<br>625 | Glu        | Asn        | Leu        | Ile        | Arg<br>630 | Val        | Phe        | Gln        | Glu        | Gly<br>635 | Arg        | Asp        | Ile        | His        | Thr<br>640 |
| Gln        | Thr        | Ala        | Ser        | Trp<br>645 | Met        | Phe        | Gly        | Val        | Pro<br>650 | Pro        | Glu        | Ala        | Val        | Asp<br>655 | Pro        |

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1647 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ATGAATTCGG | GGATGCTGCC | CCTCTTTGAG | CCCAAGGGCC | GGGTCCTCCT | GGTGGACGGC  | 60  |
| CACCACCTGG | CCTACCGCAC | CTTCCACGCC | CTGAAGGGCC | TCACCACCAG | CCGGGGGGGAG | 120 |
| CCGGTGCAGG | CGGTCTACGG | CTTCGCCAAG | AGCCTCCTCA | AGGCCCTCAA | GGAGGACGGG  | 180 |
| GACGCGGTGA | TCGTGGTCTT | TGACGCCAAG | GCCCCCTCCT | TCCGCCACGA | GGCCTACGGG  | 240 |
| GGGTACAAGG | CGGGCCGGGC | CCCCACGCCG | GAGGACTTTC | CCCGGCAACT | CGCCCTCATC  | 300 |
| AAGGAGCTGG | TGGACCTCCT | GGGGCTGGCG | CGCCTCGAGG | TCCCGGGCTA | CGAGGCGGAC  | 360 |
| GACGTCCTGG | CCAGCCTGGC | CAAGAAGGCG | GAAAAGGAGG | GCTACGAGGT | CCGCATCCTC  | 420 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| ACCGCCGACA | AAGACCTTTA | CCAGCTCCTT | TCCGACCGCA | TCCACGTCCT | CCACCCCGAG | 480  |
| GGGTACCTCA | TCACCCCGGC | CTGGCTTTTG | GAAAAGTACG | GCCTGAGGCC | CGACCAGTGG | 540  |
| GCCGACTACC | GGGCCCTGAC | CGGGGACGAG | TCCGACAACC | TTCCCGGGGT | CAAGGGCATC | 600  |
| GGGGAGAAGA | CGGCGAGGAA | GCTTCTGGAG | GAGTGGGGGA | GCCTGGAAGC | CCTCCTCAAG | 660  |
| AACCTGGACC | GGCTGAAGCC | CGCCATCCGG | GAGAAGATCC | TGGCCACAT  | GGACGATCTG | 720  |
| AAGCTCTCCT | GGGACCTGGC | CAAGGTGCGC | ACCGACCTGC | CCCTGGAGGT | GGACTTCGCC | 780  |
| AAAAGGCGGG | AGCCCGACCG | GGAGAGGCTT | AGGGCCTTTC | TGGAGAGGCT | TGAGTTTGGC | 840  |
| AGCCTCCTCC | ACGAGTTCGG | CCTTCTGGAA | AGCCCCAAGG | CCCTGGAGGA | GGCCCCCTGG | 900  |
| CCCCCGCCGG | AAGGGGCCTT | CGTGGGCTTT | GTGCTTTCCC | GCAAGGAGCC | CATGTGGGCC | 960  |
| GATCTTCTGG | CCCTGGCCGC | CGCCAGGGGG | GGCCGGGTCC | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA | GGGACCTGAA | GGAGGCGCGG | GGGCTTCTCG | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG | AAGGCCTTGG | CCTCCCGCCC | GGCGACGACC | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCTT | CCAACACCAC | CCCCGAGGGG | GTGGCCCGGC | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCGG | GGGAGCGGGC | CGCCCTTTCC | GAGAGGCTCT | TCGCCAACCT | GTGGGGGAGG | 1260 |
| CTTGAGGGGG | AGGAGAGGCT | CCTTTGGCTT | TACCGGGAGG | TGGAGAGGCC | CCTTTCCGCT | 1320 |
| GTCCTGGCCC | ACATGGAGGC | CACGGGGGTG | CGCCTGGACG | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG | TGGCCGGGGA | GATCGCCCCG | CTCGAGGCCG | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA | ACCTCAACTC | CCGGGACCAG | CTGGAAAGGG | TCCTCTTTGA | CGAGCTAGGG | 1500 |
| CTTCCCGCCA | TCGGCAAGAC | GGAGAAGACC | GGCAAGCGCT | CCACCAGCGC | CGCCGTCCTG | 1560 |
| GAGGCCCTCC | GCGAGGCCCA | CCCCATCGTG | GAGAAGATCC | TGCAGGCATG | CAAGCTTGGC | 1620 |
| ACTGGCCGTC | GTTTTACAAC | GTCGTGA    |            |            |            | 1647 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2088 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGAATTCGG | GGATGCTGCC | CCTCTTTGAG | CCCAAGGGCC | GGGTCCTCCT | GGTGGACGGC | 60  |
| CACCACCTGG | CCTACCGCAC | CTTCCACGCC | CTGAAGGGCC | TCACCACCAG | CCGGGGGGAG | 120 |
| CCGGTGCAGG | CGGTCTACGG | CTTCGCCAAG | AGCCTCCTCA | AGGCCCTCAA | GGAGGACGGG | 180 |
| GACGCGGTGA | TCGTGGTCTT | TGACGCCAAG | GCCCCCTCCT | TCCGCCACGA | GGCCTACGGG | 240 |



|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| GGGTACAAGG | CGGGCCGGGC | CCCCACGCCG | GAGGACTTTC  | CCCGGCAACT | CGCCCTCATC | 300  |
| AAGGAGCTGG | TGGACCTCCT | GGGGCTGGCG | CGCCTCGAGG  | TCCCGGGCTA | CGAGGCGGAC | 360  |
| GACGTCCTGG | CCAGCCTGGC | CAAGAAGGCG | GAAAAGGAGG  | GCTACGAGGT | CCGCATCCTC | 420  |
| ACCGCCGACA | AAGACCTTTA | CCAGCTCCTT | TCCGACCGCA  | TCCACGTCCT | CCACCCCGAG | 480  |
| GGGTACCTCA | TCACCCCGGC | CTGGCTTTTG | GAAAAGTACG  | GCCTGAGGCC | CGACCAGTGG | 540  |
| GCCGACTACC | GGGCCCTGAC | CGGGGACGAG | TCCGACAACC  | TTCCCGGGGT | CAAGGGCATC | 600  |
| GGGGAGAAGA | CGGCGAGGAA | GCTTCTGGAG | GAGTGGGGGA  | GCCTGGAAGC | CCTCCTCAAG | 660  |
| AACCTGGACC | GGCTGAAGCC | CGCCATCCGG | GAGAAGATCC  | TGGCCACAT  | GGACGATCTG | 720  |
| AAGCTCTCCT | GGGACCTGGC | CAAGGTGCGC | ACCGACCTGC  | CCCTGGAGGT | GGACTTCGCC | 780  |
| AAAAGGCGGG | AGCCCGACCG | GGAGAGGCTT | AGGGCCTTTC  | TGGAGAGGCT | TGAGTTTGGC | 840  |
| AGCCTCCTCC | ACGAGTTCGG | CCTTCTGGAA | AGCCCCAAGG  | CCCTGGAGGA | GGCCCCCTGG | 900  |
| CCCCCGCCGG | AAGGGGCCTT | CGTGGGCTTT | GTGCTTTCCC  | GCAAGGAGCC | CATGTGGGCC | 960  |
| GATCTTCTGG | CCCTGGCCGC | CGCCAGGGGG | GGCCGGGTCC  | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA | GGGACCTGAA | GGAGGCGCGG | GGGCTTCTCG  | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG | AAGGCCTTGG | CCTCCCGCCC | GGCGACGACC  | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCTT | CCAACACCAC | CCCCGAGGGG | GTGGCCCGGC  | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCGG | GGGAGCGGGC | CGCCCTTTCC | GAGAGGCTCT  | TCGCCAACCT | GTGGGGGAGG | 1260 |
| CTTGAGGGGG | AGGAGAGGCT | CCTTTGGCTT | TACCGGGAGG  | TGGAGAGGCC | CCTTTCCGCT | 1320 |
| GTCCTGGCCC | ACATGGAGGC | CACGGGGGTG | CGCCTGGACG  | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG | TGGCCGGGGA | GATCGCCCGC | CTCGAGGCCG  | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA | ACCTCAACTC | CCGGGACCAG | CTGGAAAGGG  | TCCTCTTTGA | CGAGCTAGGG | 1500 |
| CTTCCCGCCA | TCGGCAAGAC | GGAGAAGACC | GGCAAGCGCT  | CCACCAGCGC | CGCCGTCCTG | 1560 |
| GAGGCCCTCC | GCGAGGCCCA | CCCCATCGTG | GAGAAGATCC  | TGCAGTACCG | GGAGCTCACC | 1620 |
| AAGCTGAAGA | GCACCTACAT | TGACCCCTTG | CCGGACCTCA  | TCCACCCCAG | GACGGGCCGC | 1680 |
| CTCCACACCC | GCTTCAACCA | GACGGCCACG | GCCACGGGCA  | GGCTAAGTAG | CTCCGATCCC | 1740 |
| AACCTCCAGA | ACATCCCCGT | CCGCACCCCG | CTTGGGCAGA  | GGATCCGCCG | GGCCTTCATC | 1800 |
| GCCGAGGAGG | GGTGGCTATT | GGTGGCCCTG | GA CTATAGCC | AGATAGAGCT | CAGGGTGCTG | 1860 |
| GCCCACCTCT | CCGGCGACGA | GAACCTGATC | CGGGTCTTCC  | AGGAGGGGCG | GGACATCCAC | 1920 |
| ACGGAGACCG | CCAGCTGGAT | GTTCGGCGTC | CCCCGGGAGG  | CCGTGGACCC | CCTGATGCGC | 1980 |
| CGGGCGGCCA | AGACCATCAA | CTTCGGGGTC | CTCTACGGCA  | TGTCGGCCCA | CCGCCTCTCC | 2040 |
| CAGGAGCTAG | CTAGCCATCC | CTTACGAGGA | GGCCCAGGCC  | TTCATTGA   |            | 2088 |



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| ATGGAATTCTG | GGGATGCTGC | CCCTCTTTGA | GCCCAAGGGC  | CGGGTCCTCC | TGGTGGACGG | 60   |
| CCACCACCTG  | GCCTACCGCA | CCTTCCACGC | CCTGAAGGGC  | CTCACCACCA | GCCGGGGGGA | 120  |
| GCCGGTGCAG  | GCGGTCTACG | GCTTCGCCAA | GAGCCTCCTC  | AAGGCCCTCA | AGGAGGACGG | 180  |
| GGACGCGGTG  | ATCGTGGTCT | TTGACGCCAA | GGCCCCCTCC  | TTCCGCCACG | AGGCCTACGG | 240  |
| GGGGTACAAG  | GCGGGCCGGG | CCCCCACGCC | GGAGGACTTT  | CCCCGGCAAC | TCGCCCTCAT | 300  |
| CAAGGAGCTG  | GTGGACCTCC | TGGGGCTGGC | GCGCCTCGAG  | GTCCCGGGCT | ACGAGGCGGA | 360  |
| CGACGTCCTG  | GCCAGCCTGG | CCAAGAAGGC | GGAAAAGGAG  | GGCTACGAGG | TCCGCATCCT | 420  |
| CACCGCCGAC  | AAAGACCTTT | ACCAGCTCCT | TTCCGACCGC  | ATCCACGTCC | TCCACCCCGA | 480  |
| GGGGTACCTC  | ATCACCCCGG | CCTGGCTTTG | GGAAAAGTAC  | GGCCTGAGGC | CCGACCAGTG | 540  |
| GGCCGACTAC  | CGGGCCCTGA | CCGGGGACGA | GTCCGACAAC  | CTTCCCGGGG | TCAAGGGCAT | 600  |
| CGGGGAGAAG  | ACGGCGAGGA | AGCTTCTGGA | GGAGTGGGGG  | AGCCTGGAAG | CCCTCCTCAA | 660  |
| GAACCTGGAC  | CGGCTGAAGC | CCGCCATCCG | GGAGAAGATC  | CTGGCCCACA | TGGACGATCT | 720  |
| GAAGCTCTCC  | TGGGACCTGG | CCAAGGTGCG | CACCGACCTG  | CCCCTGGAGG | TGGACTTCGC | 780  |
| CAAAAGGCGG  | GAGCCCGACC | GGGAGAGGCT | TAGGGCCTTT  | CTGGAGAGGC | TTGAGTTTGG | 840  |
| CAGCCTCCTC  | CACGAGTTCG | GCCTTCTGGA | AAGCCCCAAG  | ATCCGCCGGG | CCTTCATCGC | 900  |
| CGAGGAGGGG  | TGGCTATTGG | TGGCCCTGGA | CTATAGCCAG  | ATAGAGCTCA | GGGTGCTGGC | 960  |
| CCACCTCTCC  | GGCGACGAGA | ACCTGATCCG | GGTCTTCCAG  | GAGGGGCGGG | ACATCCACAC | 1020 |
| GGAGACCGCC  | AGCTGGATGT | TCGGCGTCCC | CCGGGAGGCC  | GTGGACCCCC | TGATGCGCCG | 1080 |
| GGCGGCCAAG  | ACCATCAACT | TCGGGGTCCT | CTACGGCATG  | TCGGCCCACC | GCCTCTCCCA | 1140 |
| GGAGCTAGCC  | ATCCCTTACG | AGGAGGCCCA | GGCCTTCATT  | GAGCGCTACT | TTCAGAGCTT | 1200 |
| CCCCAAGGTG  | CGGGCCTGGA | TTGAGAAGAC | CCTGGAGGAG  | GGCAGGAGGC | GGGGGTACGT | 1260 |
| GGAGACCCTC  | TTCGGCCGCC | GCCGCTACGT | GCCAGACCTA  | GAGGCCCGGG | TGAAGAGCGT | 1320 |
| GCGGGAGGCG  | GCCGAGCGCA | TGGCCTTCAA | CATGCCCCGTC | CGGGGCACCG | CCGCCGACCT | 1380 |
| CATGAAGCTG  | GCTATGGTGA | AGCTCTTCCC | CAGGCTGGAG  | GAAATGGGGG | CCAGGATGCT | 1440 |
| CCTTCAGGTC  | CACGACGAGC | TGGTCCTCGA | GGCCCCAAAA  | GAGAGGGCGG | AGGCCGTGGC | 1500 |
| CCGGCTGGCC  | AAGGAGGTCA | TGGAGGGGGT | GTATCCCCTG  | GCCGTGCCCC | TGGAGGTGGA | 1560 |
| GGTGGGGATA  | GGGGAGGACT | GGCTCTCCGC | CAAGGAGTGA  |            |            | 1600 |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC

34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG

60

TGTATTCTAT AGTGTCACCT AAATCGAATT C

91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

19

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60

CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 70 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60  
 CTTGTTGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG 24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 46 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 50 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 969 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ATGGCTAGCA | TGACTGGTGG | ACAGCAAATG | GGTCGGATCA | ATTCGGGGAT | GCTGCCCCCTC | 60  |
| TTTGAGCCCA | AGGGCCGGGT | CCTCCTGGTG | GACGGCCACC | ACCTGGCCTA | CCGCACCTTC  | 120 |
| CACGCCCTGA | AGGGCCTCAC | CACCAGCCGG | GGGGAGCCGG | TGCAGGCGGT | CTACGGCTTC  | 180 |
| GCCAAGAGCC | TCCTCAAGGC | CCTCAAGGAG | GACGGGGACG | CGGTGATCGT | GGTCTTTGAC  | 240 |
| GCCAAGGCCC | CCTCCTTCCG | CCACGAGGCC | TACGGGGGGT | ACAAGGCGGG | CCGGGCCCCC  | 300 |
| ACGCCGGAGG | ACTTTCCCCG | GCAACTCGCC | CTCATCAAGG | AGCTGGTGGA | CCTCCTGGGG  | 360 |
| CTGGCGCGCC | TCGAGGTCCC | GGGCTACGAG | GCGGACGACG | TCCTGGCCAG | CCTGGCCAAG  | 420 |
| AAGGCGGAAA | AGGAGGGCTA | CGAGGTCCGC | ATCCTCACCG | CCGACAAAGA | CCTTTACCAG  | 480 |
| CTTCTTTCCG | ACCGCATCCA | CGTCCTCCAC | CCCGAGGGGT | ACCTCATCAC | CCCGGCCTGG  | 540 |

CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG 600  
 GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660  
 CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC 720  
 ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780  
 GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAAA GCGGGGAGCC CGACCGGGAG 840  
 AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900  
 CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCCTGGC CGTGCCCCTG GAGGTGGAGG 960  
 TGGGGATAG 969

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 948 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCTC 60  
 TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120  
 CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180  
 GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240  
 GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300  
 ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGG CCTCCTGGGG 360  
 CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420  
 AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACC GCGACAAAGA CCTTTACCAG 480  
 CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540  
 CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG 600  
 GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT 660  
 CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC 720  
 ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG 780  
 GTGCGCACCG ACCTGCCCCT GGAGGTGGAC TTCGCCAAAA GCGGGGAGCC CGACCGGGAG 840  
 AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT 900  
 CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA 948

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGCCAGGGTT | TTCCCAGTCA | CGACGTTGTA | AAACGACGGC | CAGTGAATTG | TAATACGACT | 60  |
| CACTATAGGG | CGAATTCGAG | CTCGGTACCC | GGGGATCCTC | TAGAGTCGAC | CTGCAGGCAT | 120 |
| GCAAGCTTGA | GTATTCTATA | GTGTCACCTA | AATAGCTTGG | CGTAATCATG | GTCATAGCTG | 180 |
| TTTCCTGTGT | GAAATTGTTA | TCCGCT     |            |            |            | 206 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTT GTC 43

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTTCGTC 19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

|                                                 |    |
|-------------------------------------------------|----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:        |    |
| GACGAACAAG CGAGACAGCG                           | 20 |
| (2) INFORMATION FOR SEQ ID NO:36:               |    |
| (i) SEQUENCE CHARACTERISTICS:                   |    |
| (A) LENGTH: 24 base pairs                       |    |
| (B) TYPE: nucleic acid                          |    |
| (C) STRANDEDNESS: single                        |    |
| (D) TOPOLOGY: linear                            |    |
| (ii) MOLECULE TYPE: DNA (genomic)               |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:        |    |
| TTCTGGGTTC TCTGCTCTCT GGTC                      | 24 |
| (2) INFORMATION FOR SEQ ID NO:37:               |    |
| (i) SEQUENCE CHARACTERISTICS:                   |    |
| (A) LENGTH: 43 base pairs                       |    |
| (B) TYPE: nucleic acid                          |    |
| (C) STRANDEDNESS: single                        |    |
| (D) TOPOLOGY: linear                            |    |
| (ii) MOLECULE TYPE: DNA (genomic)               |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:        |    |
| GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA | 43 |
| (2) INFORMATION FOR SEQ ID NO:38:               |    |
| (i) SEQUENCE CHARACTERISTICS:                   |    |
| (A) LENGTH: 23 base pairs                       |    |
| (B) TYPE: nucleic acid                          |    |
| (C) STRANDEDNESS: single                        |    |
| (D) TOPOLOGY: linear                            |    |
| (ii) MOLECULE TYPE: DNA (genomic)               |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:        |    |
| ACCAGAGAGC AGAGAACCCA GAA                       | 23 |
| (2) INFORMATION FOR SEQ ID NO:39:               |    |
| (i) SEQUENCE CHARACTERISTICS:                   |    |
| (A) LENGTH: 21 base pairs                       |    |
| (B) TYPE: nucleic acid                          |    |
| (C) STRANDEDNESS: double                        |    |
| (D) TOPOLOGY: linear                            |    |
| (ii) MOLECULE TYPE: DNA (genomic)               |    |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:        |    |
| AACAGCTATG ACCATGATTA C                         | 21 |



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA

20

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GCCTTATTTT | ACTTTAAAAA | TTTTCAAATG | TTTCTTTTAT | ACACAATATG | TTTCTTAGTC | 60  |
| TGAATAACCT | TTTCCTCTGC | AGTATTTTTG | AGCAGTGGCT | CCGAAGGCAC | CGTCCTCTTC | 120 |
| AAGAAGTTTA | TCCAGAAGCC | AATGCACCCA | TTAGACATAA | CCGGGAATCC | TACATGGTTC | 180 |
| CTTTTATACC | ACTGTACAGA | AATGGTGATT | TCTTTATTTT | ATCCAAAGAT | CTGGGCTATG | 240 |
| ACTATAGCTA | TCTACAAGAT | TCAGGTAAAG | TTTACTTTCT | TTCAGAGGAA | TTGCTGAATC | 300 |
| TAGTGTTACC | AATTTATTTT | GAGATAACAC | AAAACTTTA  |            |            | 339 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAA T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTGG TGTTATCTCA

20



(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA | 60  |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG                          | 157 |

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC | 60  |
| CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG | 120 |
| CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG                          | 157 |

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG  | 60  |
| TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT | 120 |
| ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG                 | 165 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA | 60  |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG                          | 157 |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA | 60  |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG                          | 157 |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA | 60  |
| TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC | 180 |
| ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GCGGCGGATG | 240 |
| GTAGGGGCGG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG | 300 |
| AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC | 360 |
| TTGTATCAGA GCCATTTA                                               | 378 |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|            |              |            |            |            |            |      |
|------------|--------------|------------|------------|------------|------------|------|
| ATGCTCCTGG | CTGTTTTGTGTA | CTGCCTGCTG | TGGAGTTTCC | AGACCTCCGC | TGGCCATTTC | 60   |
| CCTAGAGCCT | GTGTCTCCTC   | TAAGAACCTG | ATGGAGAAGG | AATGCTGTCC | ACCGTGGAGC | 120  |
| GGGGACAGGA | GTCCCTGTGG   | CCAGCTTTCA | GGCAGAGGTT | CCTGTCAGAA | TATCCTTCTG | 180  |
| TCCAATGCAC | CACTTGGGCC   | TCAATTTCCC | TTCACAGGGG | TGGATGACCG | GGAGTCGTGG | 240  |
| CCTTCCGTCT | TTTATAATAG   | GACCTGCCAG | TGCTCTGGCA | ACTTCATGGG | ATTCAACTGT | 300  |
| GGAAACTGCA | AGTTTGGCTT   | TTGGGGACCA | AACTGCACAG | AGAGACGACT | CTTGGTGAGA | 360  |
| AGAAACATCT | TCGATTTGAG   | TGCCCCAGAG | AAGGACAAAT | TTTTTGCCTA | CCTCACTTTA | 420  |
| GCAAAGCATA | CCATCAGCTC   | AGACTATGTC | ATCCCCATAG | GGACCTATGG | CCAAATGAAA | 480  |
| AATGGATCAA | CACCCATGTT   | TAACGACATC | AATATTTATG | ACCTCTTTGT | CTGGATGCAT | 540  |
| TATTATGTGT | CAATGGATGC   | ACTGCTTGGG | GGATATGAAA | TCTGGAGAGA | CATTGATTTT | 600  |
| GCCCATGAAG | CACCAGCTTT   | TCTGCCTTGG | CATAGACTCT | TCTTGTTGCG | GTGGGAACAA | 660  |
| GAAATCCAGA | AGCTGACAGG   | AGATGAAAAC | TTCACTATTC | CATATTGGGA | CTGGCGGGAT | 720  |
| GCAGAAAAGT | GTGACATTTG   | CACAGATGAG | TACATGGGAG | GTCAGCACCC | CACAAATCCT | 780  |
| AACTTACTCA | GCCCAGCATC   | ATTCTTCTCC | TCTTGGCAGA | TTGTCTGTAG | CCGATTGGAG | 840  |
| GAGTACAACA | GCCATCAGTC   | TTTATGCAAT | GGAACGCCCC | AGGGACCTTT | ACGGCGTAAT | 900  |
| CCTGGAAACC | ATGACAAATC   | CAGAACCCCA | AGGCTCCCCT | CTTCAGCTGA | TGTAGAATTT | 960  |
| TGCCTGAGTT | TGACCCAATA   | TGAATCTGGT | TCCATGGATA | AAGCTGCCAA | TTTCAGCTTT | 1020 |
| AGAAATACAC | TGGAAGGATT   | TGCTAGTCCA | CTTACTGGGA | TAGCGGATGC | CTCTCAAAGC | 1080 |
| AGCATGCACA | ATGCCTTGCA   | CATCTATATG | AATGGAACAA | TGTCCCAGGT | ACAGGGATCT | 1140 |
| GCCAACGATC | CTATCTTCCT   | TCTTCACCAT | GCATTTGTTG | ACAGTATTTT | TGAGCAGTGG | 1200 |
| CTCCGAAGGC | ACCGTCCTCT   | TCAAGAAGTT | TATCCAGAAG | CCAATGCACC | CATTGGACAT | 1260 |
| AACCGGGAAT | CCTACATGGT   | TCCTTTTATA | CCACTGTACA | GAAATGGTGA | TTTCTTTATT | 1320 |
| TCATCCAAAG | ATCTGGGCTA   | TGACTATAGC | TATCTACAAG | ATTCAGACCC | AGACTCTTTT | 1380 |
| CAAGACTACA | TTAAGTCCTA   | TTTGGAACAA | GCGAGTCGGA | TCTGGTCATG | GCTCCTTGGG | 1440 |
| GCGGCGATGG | TAGGGGCCGT   | CCTCACTGCC | CTGCTGGCAG | GGCTTGTGAG | CTTGCTGTGT | 1500 |
| CGTCACAAGA | GAAAGCAGCT   | TCCTGAAGAA | AAGCAGCCAC | TCCTCATGGA | GAAAGAGGAT | 1560 |
| TACCACAGCT | TGTATCAGAG   | CCATTTA    |            |            |            | 1587 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATGCTCCTGG CTGTTTTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTT | 60   |
| CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC | 120  |
| GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG | 180  |
| TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG | 240  |
| CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT | 300  |
| GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA | 360  |
| AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTTCCTA CCTCACTTTA  | 420  |
| GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA | 480  |
| AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT | 540  |
| TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT | 600  |
| GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTTGCG GTGGGAACAA | 660  |
| GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT | 720  |
| GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT | 780  |
| AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG | 840  |
| GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT | 900  |
| CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTAGCTGA TGTAGAATTT  | 960  |
| TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT | 1020 |
| AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC | 1080 |
| AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT | 1140 |
| GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG | 1200 |
| CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT | 1260 |
| AACCAGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT | 1320 |
| TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT | 1380 |
| CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG | 1440 |



1500  
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT 1560  
TACCACAGCT TGTATCAGAG CCATTTA 1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTGAATCTTG | TAGATAGCTA | TAGTCATAGC | CCAGATCTTT | GGATGAAATA | AAGAAATCAC | 60  |
| CATTTCTGTA | CAGTGGTATA | AAAGGAACCA | TGTAGGATTC | CCGGTTATGT | CTAATGGGTG | 120 |
| CATTGGCTTC | TGGATAAACT | TCTTGAAGAG | GACGGTG    |            |            | 157 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|              |            |            |            |            |            |     |
|--------------|------------|------------|------------|------------|------------|-----|
| CTGAATCTTG   | TAGATAGCTA | TAGTCATAGC | CCAGATCTTT | GGATGAAATA | AAGAAATCAC | 60  |
| CATTTCTGTGTA | CAGTGGTATA | AAAGGAACCA | TGTAGGATTC | CTGGTTATGT | CCAATGGGTG | 120 |
| CATTGGCTTC   | TGGATAAACT | TCTTGAAGAG | GACGGTG    |            |            | 157 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG 22

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG 20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 536 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTGGCCAA | TCTACTCCCA | GGAGCAGGGA | GGGCAGGAGC | CAGGGCTGGG | CATAAAAGTC | 60  |
| AGGGCAGAGC | CATCTATTGC | TTACATTTGC | TTCTGACACA | ACTGTGTTCA | CTAGCAACCT | 120 |
| CAAACAGACA | CCATGGTGCA | CCTGACTCCT | GAGGAGAAGT | CTGCCGTTAC | TGCCCTGTGG | 180 |
| GGCAAGGTGA | ACGTGGATGA | AGTTGGTGGT | GAGGCCCTGG | GCAGGTTGGT | ATCAAGGTTA | 240 |
| CAAGACAGGT | TTAAGGAGAC | CAATAGAAAC | TGGGCATGTG | GAGACAGAGA | AGACTCTTGG | 300 |
| GTTTCTGATA | GGCACTGACT | CTCTCTGCCT | ATTGGTCTAT | TTTCCCACCC | TTAGGCTGCT | 360 |
| GGTGGTCTAC | CCTTGGACCC | AGAGGTTCTT | TGAGTCCTTT | GGGGATCTGT | CCACTCCTGA | 420 |
| TGCTGTTATG | GGCAACCCTA | AGGTGAAGGC | TCATGGCAAG | AAAGTGCTCG | GTGCCTTTAG | 480 |
| TGATGGCCTG | GCTCACCTGG | ACAACCTCAA | GGGCACCTTT | GCCACACTGA | GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 534 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTGGCCAA | TCTACTCCCA | GGAGCAGGGA | GGGCAGGAGC | CAGGGCTGGG | CATAAAAGTC | 60  |
| AGGGCAGAGC | CATCTATTGC | TTACATTTGC | TTCTGACACA | ACTGTGTTCA | CTAGCAACCT | 120 |
| CAAACAGACA | CCATGGTGCA | TCTGACTCCT | GAGGAGGTCT | GCCGTTACTG | CCCTGTGGGG | 180 |
| CAAGGTGAAC | GTGGATGAAG | TTGGTGGTGA | GGCCCTGGGC | AGGTTGGTAT | CAAGGTTACA | 240 |
| AGACAGGTTT | AAGGAGACCA | ATAGAAACTG | GGCATGTGGA | GACAGAGAAG | ACTCTTGGGT | 300 |
| TTCTGATAGG | CACTGACTCT | CTCTGCCTAT | TGGTCTATTT | TCCCACCCTT | AGGCTGCTGG | 360 |
| TGGTCTACCC | TTGGACCCAG | AGGTTCTTTG | AGTCCTTTTG | GGATCTGTCC | ACTCCTGATG | 420 |
| CTGTTATGGG | CAACCCTAAG | GTGAAGGCTC | ATGGCAAGAA | AGTGCTCGGT | GCCTTTAGTG | 480 |
| ATGGCCTGGC | TCACCTGGAC | AACCTCAAGG | GCACCTTTGC | CACACTGAGT | GAGC       | 534 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 536 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCAGTACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT  | 360 |
| GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG | 300 |
| GTTTCTGATA GGCAGTACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT  | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60

AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60

GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120

ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC 180

TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240

CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG  | 60  |
| GAGGAGCCGG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGGC | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG                       | 340 |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGCTGACAAG AAGGAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG  | 60  |
| GAGGAGCCGG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGGC | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG                       | 340 |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCTGACAAG | AAGGAAACTC | GCTGAGACAG | CAGGGACTTT | CCACAAGGGG | ATGTTACGGG | 60  |
| GAGGTACTGG | GGAGGAGCCG | GTCGGGAACG | CCCCCTCTCT | TGATGTATAA | ATATCACTGC | 120 |
| ATTTGCTCT  | GTATTCAGTC | GCTCTGCGGA | GAGGCTGGCA | GATTGAGCCC | TGGGAGGTTC | 180 |
| TCTCCAGCAC | TAGCAGGTAG | AGCCTGGGTG | TTCCCTGCTA | GACTCTCACC | AGCACTTGGC | 240 |
| CGGTGCTGGG | CAGAGTGGCT | CCACGCTTGC | TTGCTTAAAG | ACCTCTTCAA | TAAAGCTGCC | 300 |
| ATTTTAGAAG | TAGGCTAGTG | TGTGTTCCCA | TCTCTCCTAG | CCGCCGCCTG | G          | 351 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GGCTGACAAG | AAGGAAACTC | GCTGAAACAG | CAGGGACTTT  | CCACAAGGGG | ATGTTACGGG | 60  |
| GAGGTACTGG | GAAGGAGCCG | GTCGGGAACG | CCCAC TTTCT | TGATGTATAA | ATATCACTGC | 120 |
| ATTTGCTCT  | GTATTCAGTC | GCTCTGCGGA | GAGGCTGGCA  | GATTGAGCCC | TGGGAGGTTC | 180 |
| TCTCCAGCAC | TAGCAGGTAG | AGCCTGGGTG | TTCCCTGCTA  | GACTCTCACC | AGCACTTGGC | 240 |
| CGGTGCTGGG | CAGAGTGACT | CCACGCTTGC | TTGCTTAAAG  | CCCTCTTCAA | TAAAGCTGCC | 300 |
| ATTTTAGAAG | TAAGCTAGTG | TGTGTTCCCA | TCTCTCCTAG  | CCGCCGCCTG | G          | 351 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCTGACAAG | AAGGAAACTC | GCTGAGACAG | CAGGGACTTT | CCACAAGGGG | ATGTTACGGA | 60  |
| GAGGTACTGG | GGAGGAGCCG | GTCGGGAACG | CCCCTCTCT  | TGATGTATAA | ATATCACTGC | 120 |
| ATTTGCTCT  | GTATTCAGTC | GCTCTGCGGA | GAGGCTGGCA | GATTGAGCCC | TAGGAGGTTC | 180 |
| TCTCCAGCAC | TAGCAGGTAG | AGCCTGAGTG | TTCCCTGCTA | AACTCTCACC | AGCACTTGGC | 240 |
| CGGTGCTGGG | CAGAGCGGCT | CCACGCTTGC | TTGCTTAAAG | ACCTCTTCAA | TAAAGCTGCC | 300 |
| ATTTTAGAAG | TAGGCTAGTG | TGTGTTCCCA | TCTCTCCTAG | CCGCCGCCTG | G          | 351 |



(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTGGCCAA | TCTACTCCCA | GGAGCAGGGA | GGGCAGGAGC | CAGGGCTGGG | CATAAAAGTC | 60  |
| AGGGCAGAGC | CATCTATTGC | TTACATTTGC | TTCTGACACA | ACTGTGTTCA | CTAGCAACCT | 120 |
| CAAACAGACA | CCATGGTGCA | TCTGACTCCT | GAGGAGAAGT | CTGCCGTTAC | TGCCCTGTGG | 180 |
| GGCAAGGTGA | ACGTGGATGA | AGTTGGTGGT | AAGGCCCTGG | GCAGGTTGGT | ATCAAGGTTA | 240 |
| CAAGACAGGT | TTAAGGAGAC | CAATAGAAAC | TGGGCATGTG | GAGACAGAGA | AGACTCTTGG | 300 |
| GTTTCTGATA | GGCACTGACT | CTCTCTGCCT | ATTGGTCTAT | TTTCCCACCC | TTAGGCTGCT | 360 |
| GGTGGTCTAC | CCTTGGACCC | AGAGGTTCTT | TGAGTCCTTT | GGGGATCTGT | CCACTCCTGA | 420 |
| TGCTGTTATG | GGCAACCCTA | AGGTGAAGGC | TCATGGCAAG | AAAGTGCTCG | GTGCCTTTAG | 480 |
| TGATGGCCTG | GCTCACCTGG | ACAACCTCAA | GGGCACCTTT | GCCACACTGA | GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTGGCCAA | TCTACTCCCA | GGAGCAGGGA | GGGCAGGAGC | CAGGGCTGGG | CATAAAAGTC | 60  |
| AGGGCAGAGC | CATCTATTGC | TTACATTTGC | TTCTGACACA | ACTGTGTTCA | CTAGCAACCT | 120 |
| CAAACAGACA | CCATGGTGCA | CCTGACTCCT | GAGGAGAAGT | CTGCCGTTAC | TGCCCTGTGG | 180 |
| GGCAAGGTGA | ACGTGGATGA | AGTTGGTGGT | GAGGCCCTGG | GCAGGTTGGT | ATCAAGGTTA | 240 |
| CAAGACAGGT | TTAAGGAGAC | CAATAGAAAC | TGGGCATGTG | GAGACAGAGA | AGACTCTTGG | 300 |
| GTTTCTGATA | GGCACTGACT | CTCTCTGCCT | ATTAGTCTAT | TTTCCCACCC | TTAGGCTGCT | 360 |
| GGTGGTCTAC | CCTTGGACCC | AGAGGTTCTT | TGAGTCCTTT | GGGGATCTGT | CCACTCCTGA | 420 |
| TGCTGTTATG | GGCAACCCTA | AGGTGAAGGC | TCATGGCAAG | AAAGTGCTCG | GTGCCTTTAG | 480 |
| TGATGGCCTG | GCTCACCTGG | ACAACCTCAA | GGGCACCTTT | GCCACACTGA | GTGAGC     | 536 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asp | Gln | Trp | Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Leu | Pro | Gly | Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Glu | Glu | Trp | Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Lys | Pro | Ala | Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Leu | Ser | Trp | Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Asp | Phe | Ala | Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Leu | Glu | Arg | Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Ser | Pro | Lys | Ala | Leu | Glu | Glu | Ala | Pro | Trp | Pro | Pro | Pro | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Ala | Phe | Val | Gly | Phe | Val | Leu | Ser | Arg | Lys | Glu | Pro | Met | Trp | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Leu | Leu | Ala | Leu | Ala | Ala | Ala | Arg | Gly | Gly | Arg | Val | His | Arg | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Glu | Pro | Tyr | Lys | Ala | Leu | Arg | Asp | Leu | Lys | Glu | Ala | Arg | Gly | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Ala | Lys | Asp | Leu | Ser | Val | Leu | Ala | Leu | Arg | Glu | Gly | Leu | Gly | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Pro | Gly | Asp | Asp | Pro | Met | Leu | Leu | Ala | Tyr | Leu | Leu | Asp | Pro | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asn | Thr | Thr | Pro | Glu | Gly | Val | Ala | Arg | Arg | Tyr | Gly | Gly | Glu | Trp | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Glu | Ala | Gly | Glu | Arg | Ala | Ala | Leu | Ser | Glu | Arg | Leu | Phe | Ala | Asn |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Trp | Gly | Arg | Leu | Glu | Gly | Glu | Glu | Arg | Leu | Leu | Trp | Leu | Tyr | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Val | Glu | Arg | Pro | Leu | Ser | Ala | Val | Leu | Ala | His | Met | Glu | Ala | Thr |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Gly | Val | Arg | Leu | Asp | Val | Ala | Tyr | Leu | Arg | Ala | Leu | Ser | Leu | Glu | Val |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ala | Gly | Glu | Ile | Ala | Arg | Leu | Glu | Ala | Glu | Val | Phe | Arg | Leu | Ala | Gly |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| His | Pro | Phe | Asn | Leu | Asn | Ser | Arg | Asp | Gln | Leu | Glu | Arg | Val | Leu | Phe |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Asp | Glu | Leu | Gly | Leu | Pro | Ala | Ile | Gly | Lys | Thr | Glu | Lys | Thr | Gly | Lys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |

[illegible]

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asn        | Ser        | Gly        | Met<br>5   | Leu        | Pro        | Leu        | Phe        | Glu<br>10  | Pro        | Lys        | Gly        | Arg        | Val<br>15  | Leu        |
| Leu        | Val        | Asp        | Gly<br>20  | His        | His        | Leu        | Ala        | Tyr<br>25  | Arg        | Thr        | Phe        | His        | Ala<br>30  | Leu        | Lys        |
| Gly        | Leu        | Thr<br>35  | Thr        | Ser        | Arg        | Gly        | Glu<br>40  | Pro        | Val        | Gln        | Ala        | Val<br>45  | Tyr        | Gly        | Phe        |
| Ala        | Lys<br>50  | Ser        | Leu        | Leu        | Lys        | Ala<br>55  | Leu        | Lys        | Glu        | Asp        | Gly<br>60  | Asp        | Ala        | Val        | Ile        |
| Val<br>65  | Val        | Phe        | Asp        | Ala        | Lys<br>70  | Ala        | Pro        | Ser        | Phe        | Arg<br>75  | His        | Glu        | Ala        | Tyr        | Gly<br>80  |
| Gly        | Tyr        | Lys        | Ala        | Gly<br>85  | Arg        | Ala        | Pro        | Thr        | Pro<br>90  | Glu        | Asp        | Phe        | Pro        | Arg<br>95  | Gln        |
| Leu        | Ala        | Leu        | Ile<br>100 | Lys        | Glu        | Leu        | Val        | Asp<br>105 | Leu        | Leu        | Gly        | Leu        | Ala<br>110 | Arg        | Leu        |
| Glu        | Val        | Pro<br>115 | Gly        | Tyr        | Glu        | Ala        | Asp<br>120 | Asp        | Val        | Leu        | Ala        | Ser<br>125 | Leu        | Ala        | Lys        |
| Lys        | Ala<br>130 | Glu        | Lys        | Glu        | Gly        | Tyr<br>135 | Glu        | Val        | Arg        | Ile        | Leu<br>140 | Thr        | Ala        | Asp        | Lys        |
| Asp<br>145 | Leu        | Tyr        | Gln        | Leu        | Leu<br>150 | Ser        | Asp        | Arg        | Ile        | His<br>155 | Val        | Leu        | His        | Pro        | Glu<br>160 |
| Gly        | Tyr        | Leu        | Ile        | Thr<br>165 | Pro        | Ala        | Trp        | Leu        | Trp<br>170 | Glu        | Lys        | Tyr        | Gly        | Leu<br>175 | Arg        |
| Pro        | Asp        | Gln        | Trp<br>180 | Ala        | Asp        | Tyr        | Arg        | Ala<br>185 | Leu        | Thr        | Gly        | Asp        | Glu<br>190 | Ser        | Asp        |
| Asn        | Leu        | Pro<br>195 | Gly        | Val        | Lys        | Gly        | Ile<br>200 | Gly        | Glu        | Lys        | Thr        | Ala<br>205 | Arg        | Lys        | Leu        |
| Leu        | Glu<br>210 | Glu        | Trp        | Gly        | Ser        | Leu<br>215 | Glu        | Ala        | Leu        | Leu        | Lys<br>220 | Asn        | Leu        | Asp        | Arg        |
| Leu<br>225 | Lys        | Pro        | Ala        | Ile        | Arg<br>230 | Glu        | Lys        | Ile        | Leu        | Ala<br>235 | His        | Met        | Asp        | Asp        | Leu<br>240 |
| Lys        | Leu        | Ser        | Trp        | Asp<br>245 | Leu        | Ala        | Lys        | Val        | Arg<br>250 | Thr        | Asp        | Leu        | Pro        | Leu<br>255 | Glu        |
| Val        | Asp        | Phe        | Ala<br>260 | Lys        | Arg        | Arg        | Glu        | Pro<br>265 | Asp        | Arg        | Glu        | Arg        | Leu<br>270 | Arg        | Ala        |

[illegible]

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asn        | Ser        | Gly        | Met<br>5   | Leu        | Pro        | Leu        | Phe        | Glu<br>10  | Pro        | Lys        | Gly        | Arg        | Val<br>15  | Leu        |
| Leu        | Val        | Asp        | Gly<br>20  | His        | His        | Leu        | Ala        | Tyr<br>25  | Arg        | Thr        | Phe        | His        | Ala<br>30  | Leu        | Lys        |
| Gly        | Leu        | Thr<br>35  | Thr        | Ser        | Arg        | Gly        | Glu<br>40  | Pro        | Val        | Gln        | Ala        | Val<br>45  | Tyr        | Gly        | Phe        |
| Ala        | Lys<br>50  | Ser        | Leu        | Leu        | Lys        | Ala<br>55  | Leu        | Lys        | Glu        | Asp        | Gly<br>60  | Asp        | Ala        | Val        | Ile        |
| Val<br>65  | Val        | Phe        | Asp        | Ala        | Lys<br>70  | Ala        | Pro        | Ser        | Phe        | Arg<br>75  | His        | Glu        | Ala        | Tyr        | Gly<br>80  |
| Gly        | Tyr        | Lys        | Ala        | Gly<br>85  | Arg        | Ala        | Pro        | Thr        | Pro<br>90  | Glu        | Asp        | Phe        | Pro        | Arg<br>95  | Gln        |
| Leu        | Ala        | Leu        | Ile<br>100 | Lys        | Glu        | Leu        | Val        | Asp<br>105 | Leu        | Leu        | Gly        | Leu        | Ala<br>110 | Arg        | Leu        |
| Glu        | Val        | Pro<br>115 | Gly        | Tyr        | Glu        | Ala        | Asp<br>120 | Asp        | Val        | Leu        | Ala        | Ser<br>125 | Leu        | Ala        | Lys        |
| Lys        | Ala<br>130 | Glu        | Lys        | Glu        | Gly        | Tyr<br>135 | Glu        | Val        | Arg        | Ile        | Leu<br>140 | Thr        | Ala        | Asp        | Lys        |
| Asp<br>145 | Leu        | Tyr        | Gln        | Leu        | Leu<br>150 | Ser        | Asp        | Arg        | Ile        | His<br>155 | Val        | Leu        | His        | Pro        | Glu<br>160 |
| Gly        | Tyr        | Leu        | Ile        | Thr<br>165 | Pro        | Ala        | Trp        | Leu        | Trp<br>170 | Glu        | Lys        | Tyr        | Gly        | Leu<br>175 | Arg        |
| Pro        | Asp        | Gln        | Trp<br>180 | Ala        | Asp        | Tyr        | Arg        | Ala<br>185 | Leu        | Thr        | Gly        | Asp        | Glu<br>190 | Ser        | Asp        |
| Asn        | Leu        | Pro<br>195 | Gly        | Val        | Lys        | Gly        | Ile<br>200 | Gly        | Glu        | Lys        | Thr        | Ala<br>205 | Arg        | Lys        | Leu        |
| Leu        | Glu<br>210 | Glu        | Trp        | Gly        | Ser        | Leu<br>215 | Glu        | Ala        | Leu        | Leu        | Lys<br>220 | Asn        | Leu        | Asp        | Arg        |
| Leu<br>225 | Lys        | Pro        | Ala        | Ile        | Arg<br>230 | Glu        | Lys        | Ile        | Leu        | Ala<br>235 | His        | Met        | Asp        | Asp        | Leu<br>240 |
| Lys        | Leu        | Ser        | Trp        | Asp<br>245 | Leu        | Ala        | Lys        | Val        | Arg<br>250 | Thr        | Asp        | Leu        | Pro        | Leu<br>255 | Glu        |
| Val        | Asp        | Phe        | Ala<br>260 | Lys        | Arg        | Arg        | Glu        | Pro<br>265 | Asp        | Arg        | Glu        | Arg        | Leu<br>270 | Arg        | Ala        |
| Phe        | Leu        | Glu<br>275 | Arg        | Leu        | Glu        | Phe        | Gly<br>280 | Ser        | Leu        | Leu        | His        | Glu<br>285 | Phe        | Gly        | Leu        |
| Leu        | Glu<br>290 | Ser        | Pro        | Lys        | Ala        | Leu<br>295 | Glu        | Glu        | Ala        | Pro        | Trp<br>300 | Pro        | Pro        | Pro        | Glu        |



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gly<br>305 | Ala        | Phe        | Val        | Gly        | Phe<br>310 | Val        | Leu        | Ser        | Arg        | Lys<br>315 | Glu        | Pro        | Met        | Trp        | Ala<br>320 |
| Asp        | Leu        | Leu        | Ala        | Leu<br>325 | Ala        | Ala        | Ala        | Arg        | Gly<br>330 | Gly        | Arg        | Val        | His        | Arg<br>335 | Ala        |
| Pro        | Glu        | Pro        | Tyr<br>340 | Lys        | Ala        | Leu        | Arg        | Asp<br>345 | Leu        | Lys        | Glu        | Ala        | Arg<br>350 | Gly        | Leu        |
| Leu        | Ala        | Lys<br>355 | Asp        | Leu        | Ser        | Val        | Leu<br>360 | Ala        | Leu        | Arg        | Glu        | Gly<br>365 | Leu        | Gly        | Leu        |
| Pro        | Pro<br>370 | Gly        | Asp        | Asp        | Pro        | Met<br>375 | Leu        | Leu        | Ala        | Tyr        | Leu<br>380 | Leu        | Asp        | Pro        | Ser        |
| Asn<br>385 | Thr        | Thr        | Pro        | Glu        | Gly<br>390 | Val        | Ala        | Arg        | Arg        | Tyr<br>395 | Gly        | Gly        | Glu        | Trp        | Thr<br>400 |
| Glu        | Glu        | Ala        | Gly        | Glu<br>405 | Arg        | Ala        | Ala        | Leu        | Ser<br>410 | Glu        | Arg        | Leu        | Phe        | Ala<br>415 | Asn        |
| Leu        | Trp        | Gly        | Arg<br>420 | Leu        | Glu        | Gly        | Glu<br>425 | Glu        | Arg        | Leu        | Leu        | Trp        | Leu<br>430 | Tyr        | Arg        |
| Glu        | Val        | Glu<br>435 | Arg        | Pro        | Leu        | Ser        | Ala<br>440 | Val        | Leu        | Ala        | His        | Met<br>445 | Glu        | Ala        | Thr        |
| Gly        | Val<br>450 | Arg        | Leu        | Asp        | Val        | Ala<br>455 | Tyr        | Leu        | Arg        | Ala        | Leu<br>460 | Ser        | Leu        | Glu        | Val        |
| Ala<br>465 | Gly        | Glu        | Ile        | Ala        | Arg<br>470 | Leu        | Glu        | Ala        | Glu        | Val<br>475 | Phe        | Arg        | Leu        | Ala        | Gly<br>480 |
| His        | Pro        | Phe        | Asn        | Leu<br>485 | Asn        | Ser        | Arg        | Asp        | Gln<br>490 | Leu        | Glu        | Arg        | Val        | Leu<br>495 | Phe        |
| Asp        | Glu        | Leu        | Gly<br>500 | Leu        | Pro        | Ala        | Ile        | Gly<br>505 | Lys        | Thr        | Glu        | Lys        | Thr<br>510 | Gly        | Lys        |
| Arg        | Ser        | Thr<br>515 | Ser        | Ala        | Ala        | Val        | Leu<br>520 | Glu        | Ala        | Leu        | Arg        | Glu<br>525 | Ala        | His        | Pro        |
| Ile        | Val<br>530 | Glu        | Lys        | Ile        | Leu        | Gln<br>535 | Tyr        | Arg        | Glu        | Leu        | Thr<br>540 | Lys        | Leu        | Lys        | Ser        |
| Thr<br>545 | Tyr        | Ile        | Asp        | Pro        | Leu<br>550 | Pro        | Asp        | Leu        | Ile        | His<br>555 | Pro        | Arg        | Thr        | Gly        | Arg<br>560 |
| Leu        | His        | Thr        | Arg        | Phe<br>565 | Asn        | Gln        | Thr        | Ala        | Thr<br>570 | Ala        | Thr        | Gly        | Arg        | Leu<br>575 | Ser        |
| Ser        | Ser        | Asp        | Pro<br>580 | Asn        | Leu        | Gln        | Asn        | Ile<br>585 | Pro        | Val        | Arg        | Thr        | Pro<br>590 | Leu        | Gly        |
| Gln        | Arg        | Ile<br>595 | Arg        | Arg        | Ala        | Phe        | Ile<br>600 | Ala        | Glu        | Glu        | Gly        | Trp<br>605 | Leu        | Leu        | Val        |
| Ala        | Leu<br>610 | Asp        | Tyr        | Ser        | Gln        | Ile<br>615 | Glu        | Leu        | Arg        | Val        | Leu<br>620 | Ala        | His        | Leu        | Ser        |
| Gly<br>625 | Asp        | Glu        | Asn        | Leu        | Ile<br>630 | Arg        | Val        | Phe        | Gln        | Glu<br>635 | Gly        | Arg        | Asp        | Ile        | His<br>640 |

|     |            |            |            |            |     |            |            |            |            |     |     |            |            |            |     |
|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|-----|------------|------------|------------|-----|
| Thr | Glu        | Thr        | Ala        | Ser<br>645 | Trp | Met        | Phe        | Gly        | Val<br>650 | Pro | Arg | Glu        | Ala        | Val<br>655 | Asp |
| Pro | Leu        | Met        | Arg<br>660 | Arg        | Ala | Ala        | Lys        | Thr<br>665 | Ile        | Asn | Phe | Gly        | Val<br>670 | Leu        | Tyr |
| Gly | Met        | Ser<br>675 | Ala        | His        | Arg | Leu        | Ser<br>680 | Gln        | Glu        | Leu | Ala | Ser<br>685 | His        | Pro        | Leu |
| Arg | Gly<br>690 | Gly        | Pro        | Gly        | Leu | His<br>695 |            |            |            |     |     |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|            |            |            |            |           |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asn        | Ser        | Gly        | Met<br>5  | Leu        | Pro        | Leu        | Phe        | Glu<br>10  | Pro        | Lys        | Gly        | Arg        | Val<br>15  | Leu        |
| Leu        | Val        | Asp        | Gly<br>20  | His       | His        | Leu        | Ala        | Tyr<br>25  | Arg        | Thr        | Phe        | His        | Ala<br>30  | Leu        | Lys        |
| Gly        | Leu        | Thr<br>35  | Thr        | Ser       | Arg        | Gly        | Glu<br>40  | Pro        | Val        | Gln        | Ala        | Val<br>45  | Tyr        | Gly        | Phe        |
| Ala        | Lys<br>50  | Ser        | Leu        | Leu       | Lys        | Ala<br>55  | Leu        | Lys        | Glu        | Asp        | Gly<br>60  | Asp        | Ala        | Val        | Ile        |
| Val<br>65  | Val        | Phe        | Asp        | Ala       | Lys<br>70  | Ala        | Pro        | Ser        | Phe        | Arg<br>75  | His        | Glu        | Ala        | Tyr        | Gly<br>80  |
| Gly        | Tyr        | Lys        | Ala        | Gly<br>85 | Arg        | Ala        | Pro        | Thr        | Pro<br>90  | Glu        | Asp        | Phe        | Pro        | Arg<br>95  | Gln        |
| Leu        | Ala        | Leu        | Ile<br>100 | Lys       | Glu        | Leu        | Val        | Asp<br>105 | Leu        | Leu        | Gly        | Leu        | Ala<br>110 | Arg        | Leu        |
| Glu        | Val        | Pro<br>115 | Gly        | Tyr       | Glu        | Ala        | Asp<br>120 | Asp        | Val        | Leu        | Ala        | Ser<br>125 | Leu        | Ala        | Lys        |
| Lys        | Ala<br>130 | Glu        | Lys        | Glu       | Gly        | Tyr<br>135 | Glu        | Val        | Arg        | Ile        | Leu<br>140 | Thr        | Ala        | Asp        | Lys        |
| Asp<br>145 | Leu        | Tyr        | Gln        | Leu       | Leu<br>150 | Ser        | Asp        | Arg        | Ile        | His<br>155 | Val        | Leu        | His        | Pro        | Glu<br>160 |
| Gly        | Tyr        | Leu        | Ile<br>165 | Thr       | Pro        | Ala        | Trp        | Leu        | Trp<br>170 | Glu        | Lys        | Tyr        | Gly        | Leu<br>175 | Arg        |
| Pro        | Asp        | Gln        | Trp<br>180 | Ala       | Asp        | Tyr        | Arg        | Ala<br>185 | Leu        | Thr        | Gly        | Asp        | Glu<br>190 | Ser        | Asp        |
| Asn        | Leu        | Pro<br>195 | Gly        | Val       | Lys        | Gly        | Ile<br>200 | Gly        | Glu        | Lys        | Thr        | Ala<br>205 | Arg        | Lys        | Leu        |

[illegible]

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Ala        | Ser        | Met        | Thr<br>5  | Gly        | Gly        | Gln        | Gln        | Met<br>10 | Gly        | Arg        | Ile        | Asn        | Ser<br>15 | Gly        |
| Met        | Leu        | Pro        | Leu<br>20  | Phe       | Glu        | Pro        | Lys        | Gly<br>25  | Arg       | Val        | Leu        | Leu        | Val<br>30  | Asp       | Gly        |
| His        | His        | Leu<br>35  | Ala        | Tyr       | Arg        | Thr        | Phe<br>40  | His        | Ala       | Leu        | Lys        | Gly<br>45  | Leu        | Thr       | Thr        |
| Ser        | Arg<br>50  | Gly        | Glu        | Pro       | Val        | Gln<br>55  | Ala        | Val        | Tyr       | Gly        | Phe<br>60  | Ala        | Lys        | Ser       | Leu        |
| Leu<br>65  | Lys        | Ala        | Leu        | Lys       | Glu<br>70  | Asp        | Gly        | Asp        | Ala       | Val<br>75  | Ile        | Val        | Val        | Phe       | Asp<br>80  |
| Ala        | Lys        | Ala        | Pro        | Ser<br>85 | Phe        | Arg        | His        | Glu        | Ala<br>90 | Tyr        | Gly        | Gly        | Tyr        | Lys<br>95 | Ala        |
| Gly        | Arg        | Ala        | Pro<br>100 | Thr       | Pro        | Glu        | Asp        | Phe<br>105 | Pro       | Arg        | Gln        | Leu        | Ala<br>110 | Leu       | Ile        |
| Lys        | Glu        | Leu<br>115 | Val        | Asp       | Leu        | Leu        | Gly<br>120 | Leu        | Ala       | Arg        | Leu        | Glu<br>125 | Val        | Pro       | Gly        |
| Tyr        | Glu<br>130 | Ala        | Asp        | Asp       | Val        | Leu<br>135 | Ala        | Ser        | Leu       | Ala        | Lys<br>140 | Lys        | Ala        | Glu       | Lys        |
| Glu<br>145 | Gly        | Tyr        | Glu        | Val       | Arg<br>150 | Ile        | Leu        | Thr        | Ala       | Asp<br>155 | Lys        | Asp        | Leu        | Tyr       | Gln<br>160 |

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) \delta(x-a) dx = f(a)$

[illegible]

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met<br>1  | Leu       | Pro       | Leu       | Phe<br>5  | Glu       | Pro       | Lys       | Gly       | Arg<br>10 | Val       | Leu       | Leu       | Val       | Asp<br>15 | Gly       |
| His       | His       | Leu       | Ala<br>20 | Tyr       | Arg       | Thr       | Phe       | His<br>25 | Ala       | Leu       | Lys       | Gly       | Leu<br>30 | Thr       | Thr       |
| Ser       | Arg       | Gly<br>35 | Glu       | Pro       | Val       | Gln       | Ala<br>40 | Val       | Tyr       | Gly       | Phe       | Ala<br>45 | Lys       | Ser       | Leu       |
| Leu       | Lys<br>50 | Ala       | Leu       | Lys       | Glu       | Asp<br>55 | Gly       | Asp       | Ala       | Val       | Ile<br>60 | Val       | Val       | Phe       | Asp       |
| Ala<br>65 | Lys       | Ala       | Pro       | Ser       | Phe<br>70 | Arg       | His       | Glu       | Ala       | Tyr<br>75 | Gly       | Gly       | Tyr       | Lys       | Ala<br>80 |
| Gly       | Arg       | Ala       | Pro       | Thr<br>85 | Pro       | Glu       | Asp       | Phe       | Pro<br>90 | Arg       | Gln       | Leu       | Ala       | Leu<br>95 | Ile       |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Ala | Arg | Leu | Glu | Val | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Ser | Leu | Ala | Lys | Lys | Ala | Glu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Lys | Asp | Leu | Tyr | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Leu | Ser | Asp | Arg | Ile | His | Val | Leu | His | Pro | Glu | Gly | Tyr | Leu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | Pro | Asp | Gln | Trp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asp | Tyr | Arg | Ala | Leu | Thr | Gly | Asp | Glu | Ser | Asp | Asn | Leu | Pro | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Lys | Gly | Ile | Gly | Glu | Lys | Thr | Ala | Arg | Lys | Leu | Leu | Glu | Glu | Trp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ser | Leu | Glu | Ala | Leu | Leu | Lys | Asn | Leu | Asp | Arg | Leu | Lys | Pro | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Arg | Glu | Lys | Ile | Leu | Ala | His | Met | Asp | Asp | Leu | Lys | Leu | Ser | Trp |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Asp | Leu | Ala | Lys | Val | Arg | Thr | Asp | Leu | Pro | Leu | Glu | Val | Asp | Phe | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Arg | Arg | Glu | Pro | Asp | Arg | Glu | Arg | Leu | Arg | Ala | Phe | Leu | Glu | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Glu | Phe | Gly | Ser | Leu | Leu | His | Glu | Phe | Gly | Leu | Leu | Glu | Ser | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ile | Arg | Arg | Ala | Phe | Ile | Ala | Glu | Glu | Gly | Trp | Leu | Leu | Val | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asp | Tyr | Ser | Gln | Ile | Glu | Leu | Arg | Val | Leu | Ala | His | Leu | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Glu | Asn | Leu | Ile | Arg | Val | Phe | Gln | Glu | Gly | Arg | Asp | Ile | His | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Thr | Ala | Ser | Trp | Met | Phe | Gly | Val | Pro | Arg | Glu | Ala | Val | Asp | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Met | Arg | Arg | Ala | Ala | Lys | Thr | Ile | Asn | Phe | Gly | Val | Leu | Tyr | Gly |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Met | Ser | Ala | His | Arg | Leu | Ser | Gln | Glu | Leu | Ala | Ile | Pro | Tyr | Glu | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Gln | Ala | Phe | Ile | Glu | Arg | Tyr | Phe | Gln | Ser | Phe | Pro | Lys | Val | Arg |
|     |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Trp | Ile | Glu | Lys | Thr | Leu | Glu | Glu | Gly | Arg | Arg | Arg | Gly | Tyr | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Thr | Leu | Phe | Gly | Arg | Arg | Arg | Tyr | Val | Pro | Asp | Leu | Glu | Ala | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Ser | Val | Arg | Glu | Ala | Ala | Glu | Arg | Met | Ala | Phe | Asn | Met | Pro |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Val | Arg | Gly | Thr | Ala | Ala | Asp | Leu | Met | Lys | Leu | Ala | Met | Val | Lys | Leu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | Pro | Arg | Leu | Glu | Glu | Met | Gly | Ala | Arg | Met | Leu | Leu | Gln | Val | His |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asp | Glu | Leu | Val | Leu | Glu | Ala | Pro | Lys | Glu | Arg | Ala | Glu | Ala | Val | Ala |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Arg | Leu | Ala | Lys | Glu | Val | Met | Glu | Gly | Val | Tyr | Pro | Leu | Ala | Val | Pro |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Leu | Glu | Val | Glu | Val | Gly | Ile | Gly | Glu | Asp | Trp | Leu | Ser | Ala | Lys | Glu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Ala        | Ser        | Met        | Thr<br>5  | Gly        | Gly        | Gln        | Gln        | Met<br>10 | Gly        | Arg        | Ile        | Asn        | Ser<br>15 | Gly        |
| Met        | Leu        | Pro        | Leu<br>20  | Phe       | Glu        | Pro        | Lys        | Gly<br>25  | Arg       | Val        | Leu        | Leu        | Val<br>30  | Asp       | Gly        |
| His        | His        | Leu<br>35  | Ala        | Tyr       | Arg        | Thr        | Phe<br>40  | His        | Ala       | Leu        | Lys        | Gly<br>45  | Leu        | Thr       | Thr        |
| Ser        | Arg<br>50  | Gly        | Glu        | Pro       | Val        | Gln<br>55  | Ala        | Val        | Tyr       | Gly        | Phe<br>60  | Ala        | Lys        | Ser       | Leu        |
| Leu<br>65  | Lys        | Ala        | Leu        | Lys       | Glu<br>70  | Asp        | Gly        | Asp        | Ala       | Val<br>75  | Ile        | Val        | Val        | Phe       | Asp<br>80  |
| Ala        | Lys        | Ala        | Pro        | Ser<br>85 | Phe        | Arg        | His        | Glu<br>90  | Ala       | Tyr        | Gly        | Gly        | Tyr        | Lys<br>95 | Ala        |
| Gly        | Arg        | Ala        | Pro<br>100 | Thr       | Pro        | Glu        | Asp        | Phe<br>105 | Pro       | Arg        | Gln        | Leu        | Ala<br>110 | Leu       | Ile        |
| Lys        | Glu        | Leu<br>115 | Val        | Asp       | Leu        | Leu        | Gly<br>120 | Leu        | Ala       | Arg        | Leu        | Glu<br>125 | Val        | Pro       | Gly        |
| Tyr        | Glu<br>130 | Ala        | Asp        | Asp       | Val        | Leu<br>135 | Ala        | Ser        | Leu       | Ala        | Lys<br>140 | Lys        | Ala        | Glu       | Lys        |
| Glu<br>145 | Gly        | Tyr        | Glu        | Val       | Arg<br>150 | Ile        | Leu        | Thr        | Ala       | Asp<br>155 | Lys        | Asp        | Leu        | Tyr       | Gln<br>160 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu        | Leu        | Ser        | Asp        | Arg<br>165 | Ile        | His        | Val        | Leu        | His<br>170 | Pro        | Glu        | Gly        | Tyr        | Leu<br>175 | Ile        |
| Thr        | Pro        | Ala        | Trp<br>180 | Leu        | Trp        | Glu        | Lys        | Tyr<br>185 | Gly        | Leu        | Arg        | Pro        | Asp<br>190 | Gln        | Trp        |
| Ala        | Asp        | Tyr<br>195 | Arg        | Ala        | Leu        | Thr        | Gly<br>200 | Asp        | Glu        | Ser        | Asp        | Asn<br>205 | Leu        | Pro        | Gly        |
| Val        | Lys<br>210 | Gly        | Ile        | Gly        | Glu        | Lys<br>215 | Thr        | Ala        | Arg        | Lys        | Leu<br>220 | Leu        | Glu        | Glu        | Trp        |
| Gly<br>225 | Ser        | Leu        | Glu        | Ala        | Leu<br>230 | Leu        | Lys        | Asn        | Leu        | Asp<br>235 | Arg        | Leu        | Lys        | Pro        | Ala<br>240 |
| Ile        | Arg        | Glu        | Lys        | Ile<br>245 | Leu        | Ala        | His        | Met        | Asp<br>250 | Asp        | Leu        | Lys        | Leu        | Ser<br>255 | Trp        |
| Asp        | Leu        | Ala        | Lys<br>260 | Val        | Arg        | Thr        | Asp        | Leu<br>265 | Pro        | Leu        | Glu        | Val        | Asp<br>270 | Phe        | Ala        |
| Lys        | Arg        | Arg<br>275 | Glu        | Pro        | Asp        | Arg        | Glu<br>280 | Arg        | Leu        | Arg        | Ala        | Phe<br>285 | Leu        | Glu        | Arg        |
| Leu        | Glu<br>290 | Phe        | Gly        | Ser        | Leu        | Leu<br>295 | His        | Glu        | Phe        | Gly        | Leu<br>300 | Leu        | Glu        | Ser        | Pro        |
| Lys<br>305 | Ala        | Ala        | Leu        | Glu        | His<br>310 | His        | His        | His        | His        | His<br>315 |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGAGGAGC | CGCAGTCAGA | TCCTAGCGTC | GAGCCCCCTC | TGAGTCAGGA | AACATTTTCA | 60  |
| GACCTATGGA | AACTACTTCC | TGAAAACAAC | GTTCTGTCCC | CCTTGCCGTC | CCAAGCAATG | 120 |
| GATGATTTGA | TGCTGTCCCC | GGACGATATT | GAACAATGGT | TCACTGAAGA | CCCAGGTCCA | 180 |
| GATGAAGCTC | CCAGAATGCC | AGAGGCTGCT | CCCCCGTGG  | CCCCTGCACC | AGCAGCTCCT | 240 |
| ACACCGGCGG | CCCCTGCACC | AGCCCCCTCC | TGGCCCCTGT | CATCTTCTGT | CCCTTCCCAG | 300 |
| AAAACCTACC | AGGGCAGCTA | CGGTTTCCGT | CTGGGCTTCT | TGCATTCTGG | GACAGCCAAG | 360 |
| TCTGTGACTT | GCACGTACTC | CCCTGCCCTC | AACAAGATGT | TTTGCCAACT | GGCCAAGACC | 420 |
| TGCCCTGTGC | AGCTGTGGGT | TGATTCCACA | CCCCGCCCCG | GCACCCGCGT | CCGCGCCATG | 480 |
| GCCATCTACA | AGCAGTCACA | GCACATGACG | GAGGTTGTGA | GGCGCTGCCC | CCACCATGAG | 540 |
| CGCTGCTCAG | ATAGCGATGG | TCTGGCCCCT | CCTCAGCATC | TTATCCGAGT | GGAAGGAAAT | 600 |

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| TTGCGTGTGG | AGTATTTGGA | TGACAGAAAC  | ACTTTTCGAC | ATAGTGTGGT | GGTGCCCTAT | 660  |
| GAGCCGCCTG | AGGTTGGCTC | TGACTGTACC  | ACCATCCACT | ACAACTACAT | GTGTAACAGT | 720  |
| TCCTGCATGG | GCGGCATGAA | CCGGAGGCCC  | ATCCTCACCA | TCATCACACT | GGAAGACTCC | 780  |
| AGTGGTAATC | TACTGGGACG | GAACAGCTTT  | GAGGTGCGTG | TTTGTGCCTG | TCCTGGGAGA | 840  |
| GACCGGCGCA | CAGAGGAAGA | GAATCTCCGC  | AAGAAAGGGG | AGCCTCACCA | CGAGCTGCCC | 900  |
| CCAGGGAGCA | CTAAGCGAGC | ACTGCCCCAAC | AACACCAGCT | CCTCTCCCCA | GCCAAAGAAG | 960  |
| AAACCACTGG | ATGGAGAATA | TTTCACCCTT  | CAGATCCGTG | GGCGTGAGCG | CTTCGAGATG | 1020 |
| TTCCGAGAGC | TGAATGAGGC | CTTGGAACTC  | AAGGATGCCC | AGGCTGGGAA | GGAGCCAGGG | 1080 |
| GGGAGCAGGG | CTCACTCCAG | CCACCTGAAG  | TCCAAAAAGG | GTCAGTCTAC | CTCCCGCCAT | 1140 |
| AAAAAACTCA | TGTTCAAGAC | AGAAGGGCCT  | GACTCAGACT | GA         |            | 1182 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| ATGGAGGAGC | CGCAGTCAGA | TCCTAGCGTC | GAGCCCCCTC  | TGAGTCAGGA  | AACATTTTCA | 60  |
| GACCTATGGA | AACTACTTCC | TGAAAACAAC | GTTCTGTCCC  | CCTTGCCGTC  | CCAAGCAATG | 120 |
| GATGATTTGA | TGCTGTCCCC | GGACGATATT | GAACAATGGT  | TCACTGAAGA  | CCCAGGTCCA | 180 |
| GATGAAGCTC | CCAGAATGCC | AGAGGCTGCT | CCCCCGTGG   | CCCCTGCACC  | AGCAGCTCCT | 240 |
| ACACCGGCGG | CCCCTGCACC | AGCCCCCTCC | TGGCCCCCTGT | CATCTTCTGT  | CCCTTCCCAG | 300 |
| AAAACCTACC | AGGGCAGCTA | CGGTTTCCGT | CTGGGCTTCT  | TGCATTCTGG  | GACAGCCAAG | 360 |
| TCTGTGACTT | GCACGTACTC | CCCTGCCCTC | AACAAGATGT  | TTTGCCAACT  | GGCCAAGACC | 420 |
| TGCCCTGCGC | AGCTGTGGGT | TGATTCCACA | CCCCCGCCCG  | GCACCCGCGT  | CCGCGCCATG | 480 |
| GCCATCTACA | AGCAGTCACA | GCACATGACG | GAGGTTGTGA  | GGCGCTGCCC  | CCACCATGAG | 540 |
| CGCTGCTCAG | ATAGCGATGG | TCTGGCCCCT | CCTCAGCATC  | TTATCCGAGT  | GGAAGGAAAT | 600 |
| TTGCGTGTGG | AGTATTTGGA | TGACAGAAAC | ACTTTTCGAC  | ATAGTGTGGT  | GGTGCCCTAT | 660 |
| GAGCCGCCTG | AGGTTGGCTC | TGACTGTACC | ACCATCCACT  | ACAAC TACAT | GTGTAACAGT | 720 |
| TCCTGCATGG | GCGGCATGAA | CCGGAGGCCC | ATCCTCACCA  | TCATCACACT  | GGAAGACTCC | 780 |
| AGTGGTAATC | TACTGGGACG | GAACAGCTTT | GAGGTGCGTG  | TTTGTGCCTG  | TCCTGGGAGA | 840 |
| GACCGGCGCA | CAGAGGAAGA | GAATCTCCGC | AAGAAAGGGG  | AGCCTCACCA  | CGAGCTGCCC | 900 |



960  
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGTGAGCG CTCGAGATG 1020  
 TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080  
 GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140  
 AAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA 60  
 GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG 120  
 GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA 180  
 GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCGTGG CCCCTGCACC AGCAGCTCCT 240  
 ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCTGT CATCTTCTGT CCCTTCCCAG 300  
 AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360  
 TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC 420  
 TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG 480  
 GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GCGCTGCCC CCACCATGAG 540  
 CGCTGCTCAG ATAGCGATGG TCTGGCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT 600  
 TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT 660  
 GAGCCGCCTG AGGTTGGCTC TGAAGTACC ACCATCCACT ACAACTACAT GTGTAACAGT 720  
 TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC 780  
 AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA 840  
 GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC 900  
 CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG 960  
 AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGTGAGCG CTCGAGATG 1020  
 TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG 1080  
 GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT 1140  
 AAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA 1182

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG 20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG 20

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC | 360 |
| CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA | 600 |
| C                                                                 | 601 |



TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540  
 CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600  
 C 601

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60  
 GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC 120  
 AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180  
 GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240  
 GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300  
 GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG 360  
 AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC 420  
 CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG 480  
 TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT 540  
 GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600  
 A 601

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60  
 CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC 120  
 ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180  
 GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240  
 TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA 300



(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC 24

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT 23

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTTGAG GTGCATGTTT GT 22

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCTGGGCTTC | TTGCATTCTG | GGACAGCCAA | GTCTGTGACT | TGCACGTACT | CCCCTGCCCT | 60  |
| CAACAAGATG | TTTTGCCAAC | TGGCCAAGAC | CTGCCCTGTG | CAGCTGTGGG | TTGATTCCAC | 120 |
| ACCCCCGCCC | GGCACCCGCG | TCCGCGCCAT | GGCCATCTAC | AAGCAGTCAC | AGCACATGAC | 180 |
| GGAGGTTGTG | AGGCGCTGCC | CCCACCATGA | GCGCTGCTCA | GATAGCGATG | GTCTGGCCCC | 240 |
| TCCTCAGCAT | CTTATCCGAG | TGGAAGGAAA | TTTGCGTGTG | GAGTATTTGG | ATGACAGAAA | 300 |
| CACTTTTCGA | CATAGTGTGG | TGGTGCCCTA | TGAGCCGCCT | GAGGTTGGCT | CTGACTGTAC | 360 |
| CACCATCCAC | TACAACTACA | TGTGTAACAG | TTCCTGCATG | GGCGGCATGA | ACCGGAGGCC | 420 |
| CATCCTCACC | ATCATCACAC | TGGAAGACTC | CAGTGGTAAT | CTACTGGGAC | GGAACAGCTT | 480 |
| TGAGGTGCAT | GTTTGTGCCT | GTCCTGGGAG | AGACCGGCGC | ACAGAGGAAG | AGAATCTCCG | 540 |
| CAAGAAAGGG | GAGCCTCACC | ACGAGCTGCC | CCCAGGGAGC | ACTAAGCGAG | CACTGCCCAA | 600 |
| C          |            |            |            |            |            | 601 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGGGCAGT | GCTCGCTTAG | TGCTCCCTGG | GGGCAGCTCG | TGGTGAGGCT | CCCCTTTCTT | 60  |
| GCGGAGATTC | TCTTCCTCTG | TGCGCCGGTC | TCTCCCAGGA | CAGGCACAAA | CATGCACCTC | 120 |
| AAAGCTGTTC | CGTCCCAGTA | GATTACCACT | GGAGTCTTCC | AGTGTGATGA | TGGTGAGGAT | 180 |
| GGGCCTCCGG | TTCATGCCGC | CCATGCAGGA | ACTGTTACAC | ATGTAGTTGT | AGTGGATGGT | 240 |
| GGTACAGTCA | GAGCCAACCT | CAGGCGGCTC | ATAGGGCACC | ACCACACTAT | GTCGAAAAGT | 300 |
| GTTTCTGTCA | TCCAAATACT | CCACACGCAA | ATTTCCCTTC | ACTCGGATAA | GATGCTGAGG | 360 |
| AGGGGCCAGA | CCATCGCTAT | CTGAGCAGCG | CTCATGGTGG | GGGCAGCGCC | TCACAACCTC | 420 |
| CGTCATGTGC | TGTGACTGCT | TGTAGATGGC | CATGGCGCGG | ACGCGGGTGC | CGGGCGGGGG | 480 |
| TGTGGAATCA | ACCCACAGCT | GCACAGGGCA | GGTCTTGGCC | AGTTGGCAAA | ACATCTTGTT | 540 |
| GAGGGCAGGG | GAGTACGTGC | AAGTCACAGA | CTTGGCTGTC | CCAGAATGCA | AGAAGCCCAG | 600 |
| A          |            |            |            |            |            | 601 |





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT  | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC  | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC  | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC  | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA  | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC  | 360 |
| CACCATCCAC TACAACCTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT  | 480 |
| TGAGGTGCAT GTTTGTGC                                                | 498 |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA | 60  |
| TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT | 120 |
| GCCCAAC                                                           | 127 |

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|                       |    |
|-----------------------|----|
| GGTTTTTCTT TGAGGTTTAG | 20 |
|-----------------------|----|

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTCTTCAC | GCAGAAAGCG | TCTGGCCATG | GCGTTAGTAT | GAGTGTCGTG | CAGCCTCCAG | 60  |
| GACCCCCCCT | CCCGGGAGAG | CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 120 |
| CAGGACGACC | GGGTCCTTTC | TTGGATAAAC | CCGCTCAATG | CCTGGAGATT | TGGGCGTGCC | 180 |
| CCCGCAAGAC | TGCTAGCCGA | GTAGTGTTGG | GTCGCGAAAG | GCCTTGTGGT | ACTGCCTGAT | 240 |
| AGGGTGCCTG | CGAGTGCCCC | GGGAGGTCTC | GTAGACCGTG | C          |            | 281 |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| CTGTCTTCAC | GCAGAAAGCG | TCTGGCCATG | GCGTTAGTAT | GAGTGTCTGTG | CAGCCTCCAG | 60  |
| GACCCCCCCT | CCCGGGAGAG | CCATAGTGGT | CTGCGGAACC | GGTGACTGTC  | TTCACGCAGA | 120 |
| AAGCGTCTAG | CCATGGCGTT | AGTATGAGTG | TCGTGCAGCC | TCCAGGACCC  | CCCCTCCCGG | 180 |
| GAGAGCCATA | GTGGTCTGCG | GAACCGGTGA | GTACACCGGA | ATTGCCAGGA  | CGACCGGGTC | 240 |
| CTTTCTTGGA | TCAACCCGCT | CAATGCCTGG | AGATTTGGGC | GTGCCCCCGC  | AAGACTGCTA | 300 |
| GCCGAGTAGT | GTTGGGTCGC | GAAAGGCCTT | GTGGTACTGC | CTGATAGGGT  | GCTTGCGAGT | 360 |
| GCCCCGGGAG | GTCTCGTAGA | CCGTGC     |            |             |            | 386 |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:
```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTCTTCAC | GCAGAAAGCG | TCTAGCCATG | GCGTTAGTAT | GAGTGTCGTG | CAGCCTCCAG | 60  |
| GTCCCCCCT  | CCCGGGAGAG | CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 120 |
| CAGGACGACC | GGGTCCTTTC | TTGGATCAAC | CCGCTCAATG | CCTGGAGATT | TGGGCGTGCC | 180 |
| CCCGCGAGAC | TGCTAGCCGA | GTAGTGTTGG | GTCGCGAAAG | GCCTTGTGGT | ACTGCCTGAT | 240 |
| AGGGTGCTTG | CGAGTGCCCC | GGGAGGTCTC | GTAGACCGTG | C          |            | 281 |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| CTGTCTTCAC | GCAGAAAGCG | TCTAGCCATG | GCGTTAGTAT | GAGTGTCTGTG | CAGCCTCCAG | 60  |
| GACCCCCCCT | CCCGGGAGAG | CCATAGTGGT | CTGCGGAACC | GGTGAGTACA  | CCGGAATTGC | 120 |
| CAGGACGACC | GGGTCCTTTC | GTGGATGTAA | CCCGCTCAAT | GCCTGGAGAT  | TTGGGCGTGC | 180 |
| CCCCGCAAGA | CTGCTAGCCG | AGTAGTGTTG | GGTCGCGAAA | GGCCTTGTGG  | TACTGCCTGA | 240 |
| TAGGGTGCTT | GCGAGTGCCC | CGGGAGGTCT | CGTAGACCGT | GC          |            | 282 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTCTTCAC | GCAGAAAGCG | TCTAGCCATG | GCGTTAGTAT | GAGTGTCTGA | CAGCCTCCAG | 60  |
| GGGGGGGGCT | CCCGGGAGAG | CCATAGTGGT | CTGCGGAACC | GGTGAGTACA | CCGGAATTGC | 120 |
| CGGGAAGACT | GGGTCCTTTC | TTGGATAAAC | CCACTCTATG | CCCGGCCATT | TGGGCGTGCC | 180 |
| CCCGCAAGAC | TGCTAGCCGA | GTAGCGTTGG | GTTGCGAAAG | GCCTTGTTGG | ACTGCCTGAT | 240 |
| AGGGTGCTTG | CGAGTACCCC | GGGAGGTCTC | GTAGACCGTG | C          |            | 281 |

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCGTG CAGCCTCCAG | 60  |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC | 120 |
| TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC | 180 |
| CCCGCGAGAT CACTAGCCGA GTAGTGTTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT | 240 |
| AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C                     | 281 |

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG | 120 |
| GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT | 240 |
| CATACTAACG CCATGGCCAG ACGCTTTCTG CGTGAAGACA G                     | 281 |

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG | 120 |
| GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT | 240 |
| CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G                     | 281 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTCGCGG GGGCACGCCC AAATCTCCAG | 120 |
| GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGA CCTGGAGGCT GCACGACACT | 240 |
| CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G                     | 281 |

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG | 120 |
| GCATTGAGCG GGTTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA | 180 |
| CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC | 240 |
| TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG                    | 282 |





(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG 20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC | 60  |
| CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG | 120 |
| CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC | 360 |
| CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GCGGGTGCCG | 600 |
| CTGGTCCGTA GCGAGGCCCC                                             | 620 |

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC  | 60  |
| CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTCGGCG  | 120 |
| CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC  | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC  | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC  | 360 |
| CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG  | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC  | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG  | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG  | 600 |
| CTGGTCCGTA GCGAGGCCCC                                              | 620 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC  | 60  |
| CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTTGGCG  | 120 |
| CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC  | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC  | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC  | 360 |
| CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG  | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC  | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG  | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG  | 600 |
| CTGGTCCGTA GCGAGGCCCC                                              | 620 |

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA  | 60  |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG  | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG  | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA   | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC  | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG  | 420 |
| CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT  | 480 |
| GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG  | 540 |
| TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG  | 600 |
| ACCACCGGCC GGATGTTGAT                                              | 620 |

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA  | 60  |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG  | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG  | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTGCTA   | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC  | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG  | 420 |
| CACATCCGGC CGTAGTGCGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT  | 480 |

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG 540  
 TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG 600  
 ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA 60  
 CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG 120  
 CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGCC 180  
 TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG 240  
 GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA 300  
 ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC 360  
 GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG 420  
 CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT 480  
 GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG 540  
 TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG 600  
 ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC 20

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60

ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120

GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180

GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240

CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360

CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420

GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480

ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540

TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600

CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 620 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG 60

ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120

GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180

GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240

CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360  
 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420  
 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480  
 ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540  
 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600  
 CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG 60  
 ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG 120  
 GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC 180  
 GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC 240  
 CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC 300  
 GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT 360  
 CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG 420  
 GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG 480  
 ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG 540  
 TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA 600  
 CAAGTCGGGT GGGAGGTCAA 620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG | 60  |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC | 180 |
| GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC | 300 |
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCAAGCAGA CCCTGCTGTG GCAGGATCCG  | 420 |
| GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG | 480 |
| ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA | 600 |
| CAAGTCGGGT GGGAGGTCAA                                             | 620 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60  |
| TTGTGCTTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCCAGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG | 300 |
| AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG | 600 |
| GTTCGGGTGC CATACGAGCT                                             | 620 |







GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540  
 CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG 600  
 GTTCCGGTGC CATACGAGCT 620

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC 60  
 TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA 120  
 GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG 180  
 TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC 240  
 CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG 300  
 AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC 360  
 GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG 420  
 AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA 480  
 GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC 540  
 CATTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG 600  
 GTTCCGGTGC CATACGAGCT 620

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG 20

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear





|                                                                   |      |
|-------------------------------------------------------------------|------|
| AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC | 1140 |
| CGGGAAGTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC | 1200 |
| ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG | 1260 |
| ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TCGTCTGTAG TCCGGATTGG AGTCTGCAAC | 1320 |
| TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT | 1380 |
| TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT | 1440 |
| AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGAAGTGGGT GAAGTCGTAA | 1500 |
| CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA                    | 1542 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTTTTATGGA GAGTTTGATC CTGGCTCAGA GTGAACGCTG GCGGCGTGCC TAATACATGC | 60   |
| AAGTCGAACG ATGAAGCTTC TAGCTTGCTA GAAGTGGATT AGTGGCGCAC GGGTGAGTAA | 120  |
| GGTATAGTTA ATCTGCCCTA CACAAGAGGA CAACAGTTGG AAACGACTGC TAATACTCTA | 180  |
| TACTCCTGCT TAACACAAGT TGAGTAGGGA AAGTTTTTCG GTGTAGGATG AGACTATATA | 240  |
| GTATCAGCTA GTTGGTAAGG TAATGGCTTA CCAAGGCTAT GACGCTTAAC TGGTCTGAGA | 300  |
| GGATGATCAG TCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG | 360  |
| GGAATATTGC GCAATGGGGG AAACCCTGAC GCAGCAACGC CGCGTGGAGG ATGACACTTT | 420  |
| TCGGAGCGTA AACTCCTTTT CTTAGGGAAG AATTCTGACG GTACCTAAGG AATAAGCACC | 480  |
| GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG CAAGCGTTAC TCGGAATCAC | 540  |
| TGGGCGTAAA GGGCGCGTAG GCGGATTATC AAGTCTCTTG TGAAATCTAA TGGCTTAACC | 600  |
| ATTAAACTGC TTGGGAAACT GATAGTCTAG AGTGAGGGAG AGGCAGATGG AATTGGTGGT | 660  |
| GTAGGGGTAA AATCCGTAGA TATCACCAAG AATACCCATT GCGAAGGCGA TCTGCTGGAA | 720  |
| CTCAACTGAC GCTAAGGCGC GAAAGCGTGG GGAGCAAACA GGATTAGATA CCCTGGTAGT | 780  |
| CCACGCCCTA AACGATGTAC ACTAGTTGTT GGGGTGCTAG TCATCTCAGT AATGCAGCTA | 840  |
| ACGCATTAAG TGTACCGCCT GGGGAGTACG GTCGCAAGAT TAAAACTCAA AGGAATAGAC | 900  |
| GGGGACCCGC ACAAGCGGTG GAGCATGTGG TTTAATTCGA AGATACGCGA AGAACCTTAC | 960  |
| CTGGGCTTGA TATCCTAAGA ACCTTTTAGA GATAAGAGGG TGCTAGCTTG CTAGAACTTA | 1020 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GAGACAGGTG CTGCACGGCT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT TAAGTCCCCG  | 1080 |
| AACGAGCGCA ACCCACGTAT TTAGTTGCTA ACGGTTTCGGC CGAGCACTCT AAATAGACTG | 1140 |
| CCTTCGTAAG GAGGAGGAAG GTGTGGACGA CGTCAAGTCA TCATGGCCCT TATGCCCAGG  | 1200 |
| GCGACACACG TGCTACAATG GCATATAGAA TGAGACGCAA TACCGCGAGG TGGAGCAAAT  | 1260 |
| CTATAAAATA TGTCCCAGTT CGGATTGTTC TCTGCAACTC GAGAGCATGA AGCCGGAATC  | 1320 |
| GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG  | 1380 |
| CCCGTCACAC CATGGGAGTT GATTTCCTC GAAGCCGGAA TACTAAACTA GTTACCGTCC   | 1440 |
| ACAGTGGAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT  | 1500 |
| TGGATCACCT CCT                                                     | 1513 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCCT AATACATGCA | 60  |
| AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC | 120 |
| ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACCGGAGCT AATACCGGAT | 180 |
| AATATTTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA | 240 |
| TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG | 300 |
| ACCTGAGAGG GTGATCGGCC AACTTGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC  | 360 |
| AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT | 420 |
| GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG | 480 |
| CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGTA | 540 |
| ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGGCGTA AAGCGCGCGT AGGCGGTTTT | 600 |
| TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGGAGGG TCATTGGAAA CTGGAAAAC  | 660 |
| TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCGCA GAGATATGGA | 720 |
| GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAAGCGT | 780 |
| GGGGATCAAA CAGGATTAGA TACCCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG | 840 |
| TTAGGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCTGGGGAGT  | 900 |
| ACGACCGCAA GGTGAAACT CAAAGGAATT GACGGGGACC CGCACAAGCG GTGGAGCATG  | 960 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT | 1020 |
| AGAGATAGAG CCTTCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC | 1080 |
| TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTAAG CTTAGTTGCC | 1140 |
| ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG | 1200 |
| ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA | 1260 |
| AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT | 1320 |
| AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG | 1380 |
| GTGAATACGT TCCCGGGTAT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC | 1440 |
| CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG | 1500 |
| TGAAGTCGTA ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCT      | 1555 |

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

|                                                    |    |
|----------------------------------------------------|----|
| GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCC | 46 |
|----------------------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTGACAATTA ATCATCGGCT CGTATAATGT GTGGAATTGT GAGCGGATAA CAATTTTACA | 60  |
| CAGGAAACAG CGATGAATTC GAGCTCGGTA CCCGGGGATC CTCTAGAGTC GACCTGCAGG | 120 |
| CATGCAAGCT TGGCACTGGC C                                           | 141 |

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

